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(54) **METHODS AND COMPOSITIONS FOR THE PRODUCTION OF STABLY TRANSFORMED,  
FERTILE MAIZE PLANTS AND CELLS THEREOF**

METHODEN UND ZUSAMMENSETZUNGEN FÜR DIE HERSTELLUNG VON STABIL  
TRANSFORMIERTEN, FRUCHTBAREN MAIS PFLANZEN UND ZELLEN DAFÜR

PROCEDES ET COMPOSITIONS DE PRODUCTION DE MAIS FECOND AINSIQUE DE SES  
CELLULES TRANSFORMEES DE MANIERE STABLE

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## Description

FIELD OF THE INVENTION

5 The present invention relates to reproducible systems for genetically transforming maize plants, to methods of selecting stable genetic transformants from suspensions of transformed cells, and to methods of producing fertile plants from the transformed cells. Transformation is achieved by the use of microprojectile bombardment to introduce nucleic acids into cells, and selectable and/or screenable marker systems, for example, genes which confer resistance (e.g., antibiotic, herbicide, etc.), or which contain an otherwise phenotypically observable trait. By means of the method of  
 10 the present invention stably transformed and fertile maize plants, as well as gametes and offspring of these are provided.

DESCRIPTION OF THE RELATED ART

15 Ever since the human species emerged from the hunting-gathering phase of its existence, and entered an agricultural phase, a major goal of human ingenuity and invention has been to improve crop yield and to alter and improve the characteristics of plants. In particular, man has sought to alter the characteristics of plants to make them more tasty and/or nutritious, to produce increased crop yield or render plants more adaptable to specific environments.

Up until recent times, crop and plant improvements depended on selective breeding of plants with desirable characteristics. Initial breeding success was probably accidental, resulting from observation of a plant with desirable characteristics, and use of that plant to propagate the next generation. However, because such plants had within them heterogenous genetic complements, it was unlikely that progeny identical to the parent(s) with the desirable traits would emerge. Nonetheless, advances in controlled breeding have resulted from both increasing knowledge of the mechanisms operative in hereditary transmission, and by empirical observations of results of making various parental plant  
 25 crosses.

Recent advances in molecular biology have dramatically expanded man's ability to manipulate the germplasm of animals and plants. Genes controlling specific phenotypes, for example specific polypeptides that lend antibiotic or herbicide resistance, have been located within certain germplasm and isolated from it. Even more important has been the ability to take the genes which have been isolated from one organism and to introduce them into another organism.  
 30 This transformation may be accomplished even where the recipient organism is from a different phylum, genus or species from that which donated the gene (heterologous transformation).

Attempts have been made to genetically engineer desired traits into plant genomes by introduction of exogenous genes using genetic engineering techniques. These techniques have been successfully applied in some plant systems, principally in dicotyledonous species. The uptake of new DNA by recipient plant cells has been accomplished by various means, including *Agrobacterium* infection (32), polyethylene glycol (PEG)-mediated DNA uptake (25), electroporation of protoplasts (17) and microprojectile bombardment (23). Unfortunately, the introduction of exogenous DNA into monocotyledonous species and subsequent regeneration of transformed plants has proven much more difficult than transformation and regeneration in dicotyledonous plants. Moreover, reports of methods for the transformation of monocotyledons such as maize, and subsequent production of fertile maize plants, have not been forthcoming. Consequently,  
 35 success has not been achieved in this area and commercial implementation of transformation by production of fertile transgenic plants has not been achieved. This failure has been particularly unfortunate in the case of maize, where there is a particularly great need for methods for improving genetic characteristics.

Examples of such failures to produce transgenic, fertile maize plants are described in EP-A-0 290 395, EP-A-0 334 539, and EP-A-0 348 348, as well as by Rhodes et al. (*Science* 240, 204, 1988). Though the authors of some of these publications have used microprojectile bombardment, they have nevertheless not been capable of preparing transgenic maize plants that are fertile.  
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Similarly, Klein et al. (*PNAS* 95, 4305, 1988) describes a process for delivering foreign genes into maize cells, which process makes use of microprojectile bombardment. No fertile transgenic maize plants were obtained, however.

European patent application 0 292 435 claims to provide a method for the production of transgenic, fertile maize plants. However, the proposed method makes use of transforming protoplasts and regenerating therefrom fertile plants. No fertile transgenic maize plants were obtained.  
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Problems in the development of genetically transformed monocotyledonous species have arisen in a variety of general areas. For example, there is generally a lack of methods which allow one to introduce nucleic acids into cells and yet permit efficient cell culture and eventual regeneration of fertile plants. Only limited successes have been noted.  
 55 In rice, for example, DNA transfer has only recently been reported using protoplast electroporation and subsequent regeneration of transgenic plants (41). Furthermore, in maize, transformation using protoplast electroporation has also been reported (see, e.g., 17).

However, recovery of stably transformed plants has not been reproducible. A particularly serious failure is that the

few transgenic plants produced in the case of maize have not been fertile (38). While regeneration of fertile corn plants from protoplasts has been reported (37, 39), these reported methods have been limited to the use of non-transformed protoplasts. Moreover, regeneration of plants from protoplasts is a technique which carries its own set of significant drawbacks. Even with vigorous attempts to achieve fertile, transformed maize plants, reports of success in this regard have not been forthcoming.

A transformation technique that circumvents the need to use protoplasts is microprojectile bombardment. Although transient expression of a reporter gene was detected in bombarded tobacco pollen (47), stable transformation by microprojectile bombardment of pollen has not been reported for any plant species. Bombardment of soybean apical meristems with DNA-coated gold particles resulted in chimeric plants containing transgenic sectors. Progeny containing the introduced gene were obtained at a low frequency (27). Bombardment of shoot meristems of immature maize embryos resulted in sectors of tissue expressing a visible marker, anthocyanin, the synthesis of which was triggered by the introduction of a regulatory gene (46). An analysis of cell lineage patterns in maize (28) suggests that germline transformation of maize by such an approach may be difficult.

A second major problem in achieving successful monocot transformation has resulted from the lack of efficient marker gene systems which have been employed to identify stably transformed cells. Marker gene systems are those which allow the selection of, and/or screening for, expression products of DNA. For use as assays for transformed cells, the selectable or screenable products should be those from genetic constructs introduced into the recipient cells. Hence, such marker genes can be used to identify stable transformants.

Of the more commonly used marker gene systems are gene systems which confer resistance to aminoglycosides such as kanamycin. While kanamycin resistance has been used successfully in both rice (51) and corn protoplast systems (38), it remains a very difficult selective agent to use in monocots due to high endogenous resistance (19). Many monocot species, maize, in particular, possess high endogenous levels of resistance to aminoglycosides. Consequently, this class of compounds cannot be used reproducibly to distinguish transformed from non-transformed tissue. New methods for reproducible selection of or screening for transformed plant cells are therefore needed.

Accordingly, it is clear that improved methods and/or approaches to the genetic transformation of monocotyledonous species would represent a great advance in the art. Furthermore, it would be of particular significance to provide novel approaches to monocot transformation, such as transformation of maize cells, which would allow for the production of stably transformed, fertile corn plants and progeny into which desired exogenous genes have been introduced. Furthermore, the identification of marker gene systems applicable to monocot systems such as maize would provide a useful means for applying such techniques generally. Thus, the development of these and other techniques for the preparation of stable genetically transformed monocots such as maize could potentially revolutionize approaches to monocot breeding.

### **SUMMARY OF THE INVENTION**

The present invention addresses one or more of the foregoing or other shortcomings in the prior art by providing methods and compositions for the preparation of stably transformed maize cells and subsequent regeneration of fertile, transgenic maize plants and progeny.

It is therefore a particular object of the present invention to provide techniques that will allow one to prepare transgenic, fertile maize plants which are preferably diploid and which have been stably transformed through the introduction of a desired gene into their genome.

The present invention thus relates generally to methods for the production of transgenic maize. As used herein, the term transgenic maize is intended to refer to plants that have incorporated exogenous genes or DNA sequences, including but not limited to genes or DNA sequences which are perhaps not normally present, genes not normally transcribed and translated ("expressed") in maize, or any other genes or DNA sequences which one desires to introduce into the non-transformed plant, such as genes which may normally be present in the non-transformed plant but which one desires to have altered expression.

Exemplary genes which may be introduced include, for example, DNA sequences or genes from a species other than maize, or even genes or sequences which originate with or are present in maize, but are incorporated into recipient cells by genetic engineering methods rather than classical reproduction or breeding techniques. However, the term exogenous, is also intended to refer to genes which are not normally present in the cell being transformed, or perhaps simply not present in the form, structure, etc., as found in the transforming DNA segment or gene, or genes which are normally present yet which one desires, e.g., to have overexpressed. Thus, the term "exogenous" gene or DNA is intended to refer to any gene or DNA segment that is introduced into a recipient cell, regardless of whether a similar gene may already be present in such a cell.

An initial step in the production of fertile transgenic maize plants is the obtaining of a DNA composition, e.g., vectors, plasmids, linear DNA fragments, and the like, a component of which is to be delivered to recipient monocotyledonous cells. DNA segments for use in transforming such cells will, of course, generally comprise the gene or genes

which one desires to introduce into the cells. These genes can further include structures such as promoters, enhancers, polylinkers, or even regulatory genes as desired.

The construction of vectors which may be employed in practicing the present invention is generally within the skill of the art. (See generally, refs 79, 80). Preferred constructs will generally include a plant promoter such as the CaMV 35S promoter (68), or others such as CaMV 19S (69), *nos* (70), *Adh* (71), sucrose synthase (72), those associated with the R gene complex (55), or even tissue specific promoters such as root cell promoters (73) and tissue specific enhancers (74). Constructs will also include the gene of interest along with a 3' end such as that from *Tr7* or *nos* (75), or the like. Regulatory elements such as *Adh* intron 1 (76), sucrose synthase intron (77) or TMV omega element (78), may further be included where desired.

Certain elements may find utility when incorporated into genomes, even without an associated expressible gene. For example, transposons such as *Ac*, *Ds* or *Mu* are elements which can insert themselves into genes and cause unstable mutations. This instability apparently results from subsequent excision of the element from the mutant locus during plant or seed development. For a review covering the use of transposon elements, see references 56 and 57. These elements, particularly *Ac*, may be introduced in order to inactivate (or activate) and thereby "tag" a particular trait. Once tagged, the gene with this trait may be cloned, e.g., using the transposon sequence as a PCR primer together with PCR gene cloning techniques (58,59). Once identified, the entire gene(s) for the particular trait, including control or regulatory regions where desired, may be isolated, cloned and manipulated as desired prior to re-introduction.

The generation and use of recipient cells is believed to be an important aspect of the invention. As used herein, the term "recipient cell" is intended to refer to maize cells that are receptive to transformation and subsequent regeneration into stably transformed, fertile maize plants. The inventors thus propose that not all cells present in a population of cells subjected to transforming events will be "recipient" to successful transformation and regeneration. However, it is proposed that through the application of the techniques disclosed herein, one will be enabled to obtain populations which contain sufficient numbers of recipient cells to allow for successful stable transformation and regeneration.

Certain techniques are disclosed which may enrich for recipient cells. For example, it is believed that Type II callus development, followed by manual selection and culture of friable, embryogenic tissue, results in an enrichment of recipient cells. Suspension culturing, particularly using the media disclosed in Table I herein, may also improve the ratio of recipient to non-recipient cells in any given population.

The frequency of occurrence of cells receiving DNA is believed to be low. Moreover, it is most likely that not all recipient cells receiving DNA segments will result in a transformed cell wherein the DNA is stably integrated into the plant genome and/or expressed. Some may show only initial and transient gene expression. However, it is proposed that certain cells from maize may be stably transformed through the application of the techniques disclosed herein.

The method of the present invention is directed to produce fertile, transgenic maize plants. With respect to maize, the inventors propose that many of the techniques of the invention will be applicable to maize varieties in general, whether inbred, elite inbred or hybrid varieties. It should be pointed out, though, that not all cell lines developed out of a particular variety or cross will necessarily show the same degree of stable transformability. For example, the present invention is exemplified through the use of A188 x B73 cell lines developed by standard techniques out of an A188 x B73 cross. The lines identified as SC716 and SC82 are examples of cell lines which were developed from an A188 x B73 cross as described hereinbelow. However, a number of other cell lines developed from the same cross have not as yet proven to be stably transformable. Thus, stable transformability may not be immediately apparent with some lines even from the same cross. (2 out of about 12 A188 x B73 lines have proved to be stably transformable and yield fertile transgenic plants; about 16% of the lines). Thus, where one desires to prepare transformants to a particular cross or variety, it will generally be desirable to develop several cell lines from the particular cross or variety (e.g., 8 to 10), and subject all of the lines so developed to the transformation protocols hereof.

In order to improve the ability to identify transformants, one may desire to employ a selectable or screenable marker gene as, or in addition to, the expressible gene of interest. Marker genes code for phenotypes that allow cells which express the marker gene to be distinguished from cells that do not have the marker. Such genes may encode either a selectable or screenable marker, depending on whether the marker confers a trait which one can select for by chemical means, i.e., through the use of a selective agent (e.g., an herbicide, antibiotic, or the like), or whether it is simply a trait that one can identify through observation or testing (e.g., the R-locus trait). Of course, many examples of suitable marker genes are known to the art and can be employed in the practice of the invention.

Possible selectable markers for use in connection with the present invention include but are not limited to a *neo* gene (82) which codes for kanamycin resistance and can be selected for using kanamycin, G418, etc.; a *bar* gene which codes for bialaphos resistance; a mutant EPSP synthase gene (67) which encodes glyphosate resistance; a nitrilase gene which confers resistance to bromoxynil (83); a mutant acetolactate synthase gene (ALS) which confers imidazolinone or sulphonylurea resistance (60); or a methotrexate resistant DHFR gene (61). Where a mutant EPSP synthase gene is employed, additional benefit may be realized through the incorporation of a suitable chloroplast transit peptide (CTP; see ref. 62).

Exemplary screenable markers include a  $\beta$ -glucuronidase or *uidA* gene (GUS) which encodes an enzyme for which

various chromogenic substrates are known or an R-locus gene, which encodes a product that regulates the production of anthocyanin pigments (red color) in plant tissues (59).

Included within the terms "selectable or screenable marker genes" are also genes which encode a secretable marker whose secretion can be detected as a means of identifying or selecting for transformed cells. Examples include markers which encode a secretable antigen that can be identified by antibody interaction, or even secretable enzymes which can be detected catalytically. Secretable proteins fall into a number of classes, including small, diffusible proteins detectable, e.g., by ELISA, small active enzymes detectable in extracellular solution, or proteins which are inserted or trapped in the cell wall.

Of course, in light of this disclosure, numerous other possible selectable and/or screenable marker genes will be apparent to those of skill in the art. Therefore, the foregoing discussion is intended to be exemplary rather than exhaustive. Although the present disclosure is exemplified in detail through the use of the *bar* and/or GUS genes, the applicable techniques for making and using any other screenable or selectable marker gene will be within the skill in the art in light of the present disclosure.

An illustrative embodiment of marker genes capable of being used in systems to select transformants is the *bar* gene from *Streptomyces*, such as from the *hygroscopicus* species. The *bar* gene codes for phosphinothricin acetyl transferase (PAT) that inactivates the active ingredient in the herbicide bialaphos, phosphinothricin (PPT). PPT inhibits glutamine synthetase, (29, 47) causing rapid accumulation of ammonia and cell death. Success in use of this selective system in the case of monocots was unexpected because of the major difficulties which have been encountered in transformation of cereals (36).

Where one desires to employ a bialaphos resistance gene in the practice of the invention, the inventors have discovered that a particularly useful gene for this purpose is the *bar* gene obtainable from species of *Streptomyces* (ATCC No. 21,705). The cloning of the *bar* gene has been described (29, 45) as has the use of the *bar* gene in the context of plants other than monocots (10, 11). However, in light of the techniques disclosed herein and the general recombinant techniques which are known in the art, the introduction and use of any of the foregoing or other genes is now possible.

The use of a gene from the maize R gene complex is proposed as a particularly useful screenable marker. The R gene complex in maize encodes a protein that acts to regulate the production of anthocyanin pigments in most seed and plant tissue. Maize strains can have one or as many as four R alleles which combine to regulate pigmentation in a developmental and tissue specific manner. The present inventors have applied a gene from the R gene complex to maize transformation because it is viable, it is a naturally occurring product in maize, and it is visualized without the need for additional assays. Thus, an R gene introduced into such cells will cause the expression of a red pigment and, if stably incorporated, can be visually scored as a red sector. If a maize line is dominant for the enzymatic intermediates in the anthocyanin biosynthetic pathway (C2, A1, A2, Bz1 and Bz2), but recessive at the R locus, any cell from that line can be employed as a recipient for transformation. Exemplary lines include rg-Stadler in Wisconsin 22 and TR112, a K55 derivative which is r-g, b, Pl.

The inventors further propose that R gene regulatory regions may be employed in chimeric constructs in order to provide mechanisms for controlling the expression of chimeric genes. More diversity of phenotypic expression is known at the R locus than at any other locus (63). It is contemplated that regulatory regions obtained from regions 5' to the structural R gene could be very valuable in directing the expression of genes for, e.g., insect resistance, herbicide tolerance or other protein coding regions. For the purposes of the present invention, it is believed that any of the various R gene family members may be successfully employed (e.g., P, S, Lc, etc.). However, the most preferred will generally be Sn (particularly Sn:bol3). Sn is a dominant member of the R gene complex and is functionally similar to the R and B loci in that Sn controls the tissue specific deposition of anthocyanin pigments in certain seedling and plant cells. Thus, its phenotype is similar to R.

The choice of the particular DNA segments to be delivered to the recipient cells will often depend on the purpose of the transformation. One of the major purposes of transformation of crop plants is to add some commercially desirable, agronomically important traits to the plant. Such traits include, but are not limited to, herbicide resistance, increased yields, insect and disease resistance, physical appearance, food content and makeup, etc. For example, one may desire to incorporate one or more genes encoding herbicide resistance. The *bar* and glyphosate tolerant EPSP synthase genes are good examples. A potential insect resistance gene which can be introduced includes the *Bacillus thuringiensis* crystal toxin gene (86), which may provide resistance to pests such as lepidopteran or coleopteran.

Genes encoding proteins characterized as having potential insecticidal activity, such as the cowpea trypsin inhibitor (CpTi; 88) may find use as a rootworm deterrent; genes encoding avermectin (84,85) may prove particularly useful as a corn rootworm deterrent. Furthermore, genes encoding lectins may confer insecticide properties (e.g., barley, wheat germ agglutinin, rice lectins, see ref. 81), while others may confer antifungal properties (e.g., hevein, chitinase, see, e.g., ref. 65).

It is proposed that benefits may be realized in terms of increased resistance to cold temperatures through the introduction of an "antifreeze" protein such as that of the Winder Flounder (87).

Ultimately, the most desirable "traits" for introduction into a maize genome may be homologous genes or gene families which encode a desired trait (e.g., increased yield per acre) and which are introduced under the control of novel promoters or enhancers, etc., or perhaps even homologous or tissue specific (e.g., root specific) promoters or control elements.

The invention thus contemplates that particular benefits may be realized by the transformation of maize cells with any expressible gene, and is not intended to be limited to the use of marker genes. As used herein, an "expressible gene" is any gene that is capable of being translated into a protein, expressed as a trait of interest or the like, etc., and is not limited to selectable, screenable or non-selectable marker genes. The invention also contemplates that, where both an expressible gene that is not necessarily a marker gene is employed in combination with a marker gene, one may employ the separate genes on either the same or different DNA segments for transformation. In the latter case, the different vectors are delivered concurrently to recipient cells to maximize cotransformation.

In certain embodiments, recipient cells are selected following growth in culture. Where employed, cultured cells will preferably be grown either on solid supports or in the form of liquid suspensions. In either instance, nutrients may be provided to the cells in the form of media, and environmental conditions controlled. There are many types of tissue culture media comprising amino acids, salts, sugars, hormones and vitamins. Most of the media employed in the practice of the invention will have some similar components (see, e.g., Table 1 herein below), the media differ in the composition and proportions of their ingredients depending on the particular application envisioned. For example, various cell types usually grow in more than one type of media, but will exhibit different growth rates and different morphologies, depending on the growth media. In some media, cells survive but do not divide.

Various types of media suitable for culture of maize plant cells have been previously described. Examples of these media include, but are not limited to the N6 medium described by Chu, et al. (5) and the MS media (30). In an exemplary embodiment for preparation of recipient cells, the inventors have modified these media (see, Table 1). A preferred hormone for such purposes is dicamba or 2,4-D. However, other hormones may be employed, including NAA or NAA + 2,4-D. Modifications of these and other basic media may facilitate growth of recipient cells at specific developmental stages.

An exemplary embodiment for culturing recipient corn cells in suspension cultures includes using embryogenic cells in Type II callus, selecting for small (10-30  $\mu$ ) isodiametric, cytoplasmically dense cells, growing the cells in suspension cultures with hormone containing media, subculturing into a progression of media to facilitate development of shoots and roots, and finally, hardening the plant and readying it metabolically for growth in soil. For use in transformation, suspension culture cells may be cryopreserved and stored for periods of time, thawed, then used as recipient cells for transformation.

An illustrative embodiment of cryopreservation methods comprises the steps of slowly adding cryoprotectants to suspension cultures to give a final concentration of 10% dimethyl sulfoxide, 10% polyethylene glycol (6000MW), 0.23 M proline, and 0.23 M glucose. The mixture is then cooled to -35°C at 0.5°C per minute. After an isothermal period of 45 minutes, samples are placed in liquid N<sub>2</sub>. (Modification of methods of Withers and King (49); and Finkle, et al. (15)). To reinitiate suspension cultures from cryopreserved material, cells may be thawed rapidly and pipetted onto feeder plates similar to those described by Rhodes, et al. (38).

One embodiment of cultured maize plant cells that can serve as recipient cells for transforming with desired DNA segments, such as those which comprise expressible genes, includes cells from *Zea mays* L. Somatic cells are of various types. Embryogenic cells are one example of somatic cells which may be induced to regenerate a plant through embryo formation. Non-embryogenic cells are those which will typically not respond in such a fashion. An example of non-embryogenic cells are certain Black Mexican Sweet (BMS) corn cells, and these have been successfully transformed by microprojectile bombardment using the *neo* gene followed by selection with the aminoglycoside, kanamycin (22). However, this BMS culture was not found to be regenerable, and general use of kanamycin may be hampered by endogenous resistance of maize (19).

Other recipient cell targets include, but are not limited to, meristem cells, Type I and II calli and gametic cells such as microspores and pollen. Pollen, as well as its precursor cells, microspores, may be capable of functioning as recipient cells for genetic transformation, or as vectors to carry foreign DNA for incorporation during fertilization. Direct pollen transformation would obviate the need for cell culture. Meristematic cells (i.e., plant cells capable of continual cell division and characterized by an undifferentiated cytological appearance, normally found at growing points or tissues in plants such as root tips, stem apices, lateral buds, etc.) may represent another type of recipient plant cell. Because of their undifferentiated growth and capacity for organ differentiation and totipotency, a single transformed meristematic cell could be recovered as a whole transformed plant. In fact, it is proposed that embryogenic suspension cultures may be an *in vitro* meristematic cell system, retaining an ability for continued cell division in an undifferentiated state, controlled by the media environment.

The development of embryogenic maize calli and suspension cultures useful in the context of the present invention, e.g., as recipient cells for transformation, has been described in U.S. Serial No. 06/877,033, filed 06/07/86, incorporated herein by reference.

There are many methods for introducing transforming DNA segments into cells, but not all are suitable for delivering DNA to plant cells. Suitable methods are believed to include virtually any method by which DNA can be introduced into a cell, such as by *Agrobacterium* infection or direct delivery of DNA such as, for example, by PEG-mediated transformation, by electroporation or by acceleration of DNA coated particles, etc. Acceleration methods are generally preferred and include, for example, microprojectile bombardment and the like. Electroporation has been used to transform corn protoplasts (17).

The method for delivering transforming DNA segments to maize cells according to the invention is microprojectile bombardment. In this method, non-biological particles may be coated with nucleic acids and delivered into cells by a propelling force. Exemplary particles include those comprised of tungsten, gold, platinum, and the like.

A particular advantage of microprojectile bombardment, in addition to it being an effective means of reproducibly stably transforming maize plants, is that neither the isolation of protoplasts (8) nor the susceptibility of *Agrobacterium* infection is required. An illustrative embodiment of a method for delivering DNA into maize cells by acceleration is a Biolistics Particle Delivery System, which can be used to propel particles coated with DNA through a screen, such as a stainless steel or Nyltex screen, onto a filter surface covered with corn cells cultured in suspension.

For the bombardment, cells in suspension are preferably concentrated on filters. Filters containing the cells to be bombarded are positioned at an appropriate distance below the macroprojectile stopping plate. If desired, one or more screens are also positioned between the gun and the cells to be bombarded. Through the use of techniques set forth herein one may obtain up to 1000 or more clusters of cells transiently expressing a marker gene ("foci") on the bombarded filter. The number of cells in a focus which express the exogenous gene product 48 hours post-bombardment often range from 1 to 10 and average 2 to 3.

After effecting delivery of exogenous DNA to recipient cells by the methods discussed above, a preferred step is to identify the transformed cells for further culturing and plant regeneration. This step may include assaying cultures directly for a screenable trait or by exposing the bombarded cultures to a selective agent or agents.

An example of a screenable marker trait is the red pigment produced under the control of the R-locus in maize. This pigment may be detected by culturing cells on a solid support containing nutrient media capable of supporting growth at this stage, incubating the cells at e.g., 18° C. and greater than 180  $\mu\text{E m}^{-2} \text{ sec}^{-1}$ , and selecting cells from colonies (visible aggregates of cells) that are pigmented. These cells may be cultured further, either in suspension or on solid media.

An exemplary embodiment of methods for identifying transformed cells involves exposing the bombarded cultures to a selective agent, such as a metabolic inhibitor, an antibiotic, herbicide or the like. Cells which have been transformed and have stably integrated a marker gene conferring resistance to the selective agent used, will grow and divide in culture. Sensitive cells will not be amenable to further culturing.

To use the bar-bialaphos selective system, bombarded cells on filters are resuspended in nonselective liquid medium, cultured (e.g., for one to two weeks) and transferred to filters overlaying solid medium containing from 1-3 mg/l bialaphos. While ranges of 1-3 mg/l will typically be preferred, it is proposed that ranges of 0.1-50 mg/l will find utility in the practice of the invention. The type of filter for use in bombardment is not believed to be particularly crucial, and can comprise any solid, porous, inert support.

Cells that survive the exposure to the selective agent may be cultured in media that supports regeneration of plants. An example of suitable media is a modification of MS media (Table 1). Tissue is maintained on a basic media with hormones for about 2-4 weeks, then transferred to media with no hormones. After 2-4 weeks, shoot development will signal the time to transfer to another media.

Regeneration typically requires a progression of media whose composition has been modified to provide the appropriate nutrients and hormonal signals during sequential developmental stages from the transformed callus to the more mature plant. Developing plantlets are transferred to soil, and hardened, e.g., in an environmentally controlled chamber at about 85% relative humidity, 600 ppm  $\text{CO}_2$ , and 250 microeinsteins  $\text{m}^{-2} \cdot \text{s}^{-1}$  of light. Plants are preferably matured either in a growth chamber or greenhouse. Regeneration will typically take about 3-12 weeks. During regeneration, cells are grown on solid media in tissue culture vessels. An illustrative embodiment of such a vessel is a petri dish. Regenerating plants are preferably grown at about 19 to 28°C. After the regenerating plants have reached the stage of shoot and root development, they may be transferred to a greenhouse for further growth and testing.

To confirm the presence in the regenerating plants of traits delivered to the recipient cells through the application of exogenous DNA, alone or in conjunction with marker genes, assays for expression of said genes may be performed, e.g., by testing parts of the regenerated plants. Exemplary parts which may be assayed are leaves. A typical transformant assay includes contacting regenerating plants or extracts of plants with a substrate that is acted upon by the transforming gene product. At this stage of development, the plants will not be lethally affected by such an assay. Removal of small portions of the plants does not cause their death or interfere with further development.

In one study,  $R_0$  plants were regenerated from transformants of an A188 x B73 suspension culture line (SC82) and these plants exhibited a phenotype expected of the genotype of hybrid A188 X B73 from which the callus and culture were derived. The plants were similar in height to seed-derived A188 plants (3-5 ft tall) but had B73 traits such



as anthocyanin accumulation in stalks and prop roots, and the presence of upright leaves. It would also be expected that some traits in the transformed plants would differ from their source, and indeed some variation will likely occur.

In an exemplary embodiment, the proportion of regenerating plants derived from transformed callus that successfully grew and reached maturity after transfer to the greenhouse was 97% (73 of 76). In one example, at least 50 viable progeny were recovered from  $R_0$  plants.  $R_0$  plants in the greenhouse were tested for fertility by backcrossing the transformed plants with seed-derived plants by pollinating the  $R_0$  ears with pollen from seed derived B73 plants and this resulted in kernel development. Note, however, that kernels on transformed plants may require embryo rescue due to cessation of kernel development and premature senescence of plants.

To rescue developing embryos, they are excised from surface-disinfected kernels 10-20 days post-pollination and cultured. An embodiment of media used for culture at this stage comprises MS salts, 2% sucrose, and 5.5 g/l agarose. In an illustrative embodiment of embryo rescue, large embryos (defined as greater than 3 mm in length) are germinated directly on an appropriate media. Embryos smaller than that were cultured for one week on media containing the above ingredients along with  $10^{-5}$ M abscisic acid and then transferred to hormone-free medium for germination.

Progeny may be recovered from the transformed plants and tested for expression of the exogenous expressible gene by localized application of an appropriate substrate to plant parts such as leaves. In the case of bar transformed plants, it was found that transformed parental plants ( $R_0$ ) and their progeny ( $R_1$ ) exhibited no bialaphos-related necrosis after localized application of the herbicide Basta to leaves, if there was functional PAT activity in the plants as assessed by an *in vitro* enzymatic assay. In one study, of 28 progeny ( $R_1$ ) plants tested, 50% (N=14) had PAT activity. All PAT positive progeny tested contained *bar*, confirming that the presence of the enzyme and the resistance to bialaphos were associated with the transmission through the germline of the marker gene. The nonchimeric nature of the callus and the parental transformants ( $R_0$ ) was suggested by germline transmission and the identical Southern blot hybridization patterns and intensities of the transforming DNA in callus,  $R_0$  plants and  $R_1$  progeny that segregated for the transformed gene.

Genomic DNA may be isolated from callus cell lines and plants to determine the presence of the exogenous gene through the use of techniques well known to those skilled in the art. Note, that intact sequences will not always be present, presumably due to rearrangement or deletion of sequences in the cell.

The inventors have been successful in producing fertile transgenic maize plants where others have failed. Aspects of the methods of the present invention for producing the fertile, transgenic corn plants comprise, but are not limited to, development of suspension cultures of recipient cells using media conducive to specific growth patterns, choice of selective systems that permit efficient detection of transformation; modifications of acceleration methods to introduce genetic vectors with exogenous DNA into cells; invention of methods to regenerate plants from transformed cells at a high frequency; and the production of fertile transgenic plants capable of surviving and reproducing.

## DEFINITIONS

Callus - Proliferating mass of cells or tissue *in vitro*.

Type I - A compact, slow growing, heteromorphic callus (embryogenic/organogenic) which retains meristematic activity in regions of organized tissue.

Type II - A friable, fast growing embryogenic callus composed of aggregates of small isodiametric cells with dense cytoplasm. Often contains small embryoids attached to the underlying callus by a suspensor.

Embryogenic Callus - A type of callus capable of differentiating into somatic embryos.

Germinal Cells (Gametes) - Cells of an organism which are capable of transferring their genetic information to the next generation.

Genotype - The genetic complement of an organism.

Heterologous DNA - DNA from a source different than that of the recipient cell.

Homologous DNA - DNA from the same source as that of the recipient cell.

Hybrid - Progeny resulting from a cross between parental lines.

Inbred Lines - Organisms that are genetically homogeneous (homozygous) resulting from many generations of self crossing.

In Vitro - In the laboratory.

In Vivo - In the living organism.

Monocot - Plants having a single cotyledon (the first leaf of the embryo of seed plants); examples include cereals such as maize, rice, wheat, oats and barley.

Non-Embryogenic Callus - A type of callus composed of undifferentiated, often highly vacuolated cells which are unable to be induced to form embryos.

Phenotype - Traits exhibited by an organism resulting from the interaction of genotype and environment.

Protoplast - Plant cells exclusive of the cell walls.

Somatic Cells - Body cells of an organism, exclusive of germinal cells.

Transformation - Acquisition of new genetic coding sequences by the incorporation of added (exogenous) DNA.

Transgenic - Organisms (plants or animals) into which new DNA sequences are integrated.

## BRIEF DESCRIPTION OF THE DRAWINGS

FIG. 1. Schematic representation of plasmids (vectors) used in bombardment experiments. The plasmids have been named (A) pDPG165 which contains *bar*, and (B) pDPG208 which contains *uidA* (the gene which encodes  $\beta$ -glucuronidase (GUS)). Letters designate the locations of various restriction sites, locations which may be cleaved by restriction endonucleases, E, EcoRI; H, HindIII; B, BamHI; S, SmaI. A more detailed map of pDPG165 is shown in (C), of pDPG208 in (D). In (E) is shown a restriction map of pAGUS1, also known as pDPG141, in which the 5'-noncoding and 5'-coding sequences were modified to incorporate the Kozak consensus sequence and a HindIII restriction site. In (F) is shown a restriction map of pDPG237, a plasmid which contains *Sn:bol3* cDNA, and in (G) is shown a map of pDPG232, a plasmid which incorporates *Rsn* cDNA along with a 35S promoter and a Tr7 3' end.

FIG. 2. Appearance of cell colonies which emerge on selection plates with bialaphos. Such colonies appear 6-7 weeks after bombardment. (A) SC82 bialaphos-resistant colony selected on 1 mg/l bialaphos. (B) Embryogenic SC82 bialaphos-resistant callus selected and maintained on 1 mg/l bialaphos.

FIG. 3. Phosphinothricin acetyl transferase (PAT) activity in embryogenic SC82 callus transformants designated E1-E11 and a nonselected control (EO). 25  $\mu$ g of protein extract were loaded per lane. B13 is a BMS-*bar* transformant. BMS is Black Mexican Sweet corn. Activities of the different transformants varied approximately 10 fold based on the intensities of the bands.

FIG. 4. Integration of the *bar* gene in bialaphos-resistant SC82 callus isolates E1-E11. DNA gel blot of genomic DNA (4  $\mu$ g/digest) from E1-E11 and a nonselected control (EO) digested with EcoRI and HindIII. The molecular weights in kb are shown on the left and right. The blot was hybridized with  $^{32}$ P-labeled *bar* from pDPG165 (-25x10<sup>6</sup> Cerenkov cpm). Lanes designated 1 and 5 copies refer to the diploid genome and contain 1.9 and 9.5 pg respectively of the 1.9 kb *bar* expression unit released from pDPG165 with EcoRI and HindIII.

FIG. 5. PAT Activity in Protein Extracts of  $R_0$  Plants. Extracts from one plant derived from each of the four transformed regenerable callus lines from a suspension culture of A188 x B73, SC82 (E10, E11, E2/E5, and E3/E4/E6) were tested for PAT activity (The designations E2/E5 and E3/E4/E6 represent transformed cell lines with identical DNA gel blot hybridization patterns; the isolates were most likely separated during the culturing and selection process.) Protein extracts from a nontransformed B73 plant and a Black Mexican Sweet (BMS) cell culture *bar* transformant were included as controls. Approximately 50 micrograms of total protein was used per reaction.

FIG. 6. DNA Gel Blot Analysis of Genomic DNA from Transformed Callus and Corresponding  $R_0$  Plants Probed with *bar*. Genomic DNA was digested with EcoRI and HindIII, which released the 1.9 kb *bar* expression unit (CaMV 35S promoter-*bar*-Tr7 3'-end) from pDPG165, the plasmid used for microprojectile bombardment transformation of SC82 cells, and hybridized to *bar*. The molecular weights in kb are shown on the left and right. Lanes designated E3/E4/E6, E11, E2/E5, and E10 contained 5  $\mu$ g of either callus (C) or  $R_0$  plant DNA. The control lane contained DNA from a nontransformed A188 X B73 plant. The lane designated "1 copy" contained 2.3 pg of the 1.9 kb EcoRI/HindIII fragment from pDPG165 representing one copy per diploid genome.

FIG. 7. PAT Activity and DNA Gel Blot Analysis of Segregating Progeny of E2/E5  $R_0$  Plants. (A) Analysis of PAT activity in ten progeny (lanes a-j) and a nontransformed control plant (lane k). Lanes designated a, b-h, i, and j contained protein extracts from progeny of separate parental  $R_0$  plants. The lane designated callus contained protein extract from E2/E5 callus. Approximately 25 micrograms of total protein were used per reaction. (B) DNA gel blot analysis of genomic DNA isolated from the ten progeny analyzed in A. Genomic DNA (5  $\mu$ g/lane) was digested with SmaI, which releases a 0.6 kb fragment containing *bar* from pDPG165, and hybridized with *bar* probe. The lane designated  $R_0$  contained DNA from the  $R_0$  parent of progeny a. The lane designated 1 copy contained pDPG165 digested with SmaI to represent approximately 1 copy of the 0.6 kb fragment per diploid genome (0.8 pg).

FIG. 8. Histochemical determination of GUS activity in *bar*-transformed SC82 callus line Y13. This bialaphos-resistant callus line, Y13, which contained intact GUS coding sequences was tested for GUS activity three months post-bombardment. In this figure, differential staining of the callus was observed.

FIG. 9. Integration of exogenous genes in bialaphos-resistant SC716 isolates R1-R21. (A) DNA gel blot of genomic DNA (6  $\mu$ g/digest) from transformants isolated from suspension culture of A188 x B73 (SC716), designated R1-R21, were digested with EcoRI and HindIII and hybridized to  $^{32}$ P-labeled *bar* probe (~10x10<sup>6</sup> Cerenkov cpm). Molecular weight markers in kb are shown on the left and right. Two copies of the *bar* expression unit per diploid genome is 5.7 pg of the 1.9 kb EcoRI/hind fragment from pDPG165. (B) The blot from A was washed and hybridized with  $^{32}$ P-labelled GUS probe (-35x10<sup>6</sup> Cerenkov cpm). Two copies of the 2.1 kb GUS-containing EcoRI/HindIII fragment from pDPG208

is 6.3 pg.

FIG. 10. Functional Expression of Introduced Genes in Transformed  $R_0$  and  $R_1$  Plants. (A) Basta<sup>R</sup> resistance in transformed  $R_0$  plants. A Basta<sup>R</sup> solution was applied to a large area (about 4 x 8 cm) in the center of leaves of nontransformed A188 x B73 plant (left) and a transgenic  $R_0$  E3/E4/E6 plant (right). (B) Basta<sup>R</sup> resistance in transformed  $R_1$  plants. Basta<sup>R</sup> was also applied to leaves of four  $R_1$  plants; two plants without *bar* (left) and two plants containing *bar* (right). The herbicide was applied to  $R_1$  plants in 1 cm circles to four locations on each leaf, two on each side of the midrib. Photographs were taken six days after application. (C) GUS activity in leaf tissue of a transgenic  $R_0$  plant. Histochemical determination of GUS activity in leaf tissue of a plant regenerated from cotransformed callus line Y13 (right) and a nontransformed tissue culture derived plant (left). Bar = 1 cm. (D) Light micrograph of the leaf segment from a Y13 plant shown in (C), observed in surface view under bright field optics. GUS activity was observed in many cell types throughout the leaf tissue (magnification = 230X). (E) Light micrograph as in (D) of control leaf.

FIG. 11. Mature  $R_0$  Plant, Developing Kernels and Progeny. (A) Mature transgenic  $R_0$  plant regenerated from an E2/E5 callus. (B) Progeny derived from an E2/E5 plant by embryo rescue; segregant bearing the resistance gene on the right, and lacking the gene on the left. (C) Using pollen from transformed  $R_1$  plants to pollinate B73 ears, large numbers of seed have been recovered. (D) A transformed ear from an  $R_1$  plant crossed with pollen from a non-transformed inbred plant.

## **DESCRIPTION OF THE PREFERRED EMBODIMENTS**

For the first time, fertile transgenic maize plants have been produced, opening the door to new vistas of crop improvement based on in vitro genetic transformation. The inventors have succeeded where others have failed by combining and modifying numerous steps in the overall process leading from somatic cell to transgenic plant. Although the methods disclosed herein are part of a unified process, for illustrative purposes they may be subdivided into: culturing cells to be recipients for exogenous DNA; cryopreserving recipient cells; constructing vectors to deliver the DNA to cells; delivering DNA to cells; assaying for successful transformations; using selective agents if necessary to isolate stable transformants; regenerating plants from transformants; assaying those plants for gene expression and for identification of the exogenous DNA sequences; determining whether the transgenic plants are fertile; and producing offspring of the transgenic plants.

### **A. Tissue Culture**

Tissue culture requires media and controlled environments. "Media" refers to the numerous nutrient mixtures that are used to grow cells in vitro, that is, outside of the intact living organism. The medium is usually a suspension of various categories of ingredients (salts, amino acids, hormones, sugars, buffers) that are required for growth of most cell types. However, each specific cell type requires a specific range of ingredient proportions for growth, and an even more specific range of formulas for optimum growth. Rate of cell growth will also vary among cultures initiated with the array of media that permit growth of that cell type.

Nutrient media is prepared as a liquid, but this may be solidified by adding the liquid to materials capable of providing a solid support. Agar is most commonly used for this purpose. Bactoagar and Gelgro are specific types of solid support that are suitable for growth of plant cells in tissue culture.

Some cell types will grow and divide either in liquid suspension or on solid media. As disclosed herein, maize cells will grow in suspension, but regeneration of plants requires transfer from liquid to solid media at some point in development. The type and extent of differentiation of cells in culture will be affected not only by the type of media used and by the environment, for example, pH, but also by whether media is solid or liquid. Table 1 illustrates the composition of various media useful for creation of recipient cells and for plant regeneration.

### **B. Culturing Cells in Suspension to be Recipients for Transformation**

It is believed by the inventors that the ability to prepare and cryopreserve suspension cultures of maize cells is an important aspect of the present invention, in that it provides a means for reproducibly and successfully preparing cells for transformation. The studies described below set forth techniques which have been successfully applied by the inventors to generate transformable and regenerable suspension cultures of maize cells. A variety of different types of media have been developed by the inventors and employed in carrying out various aspects of the invention, including in particular, the development of suspension cultures. The following table, Table 1, sets forth the composition of the media preferred by the inventors for carrying out these aspects of the invention.

Table 1:

**Illustrative Embodiments of Tissue Culture Media Which are Used for Type II Callus Development, Development of Suspension Cultures and Regeneration of Maize Plant Cells**

Medium					
Id. Number	MS*	N6	Sucrose	Optimal pH	Other Components**
52	+	-	2%	6.0	0.25 mg thiamine 1 mg 2,4-D 10 <sup>-7</sup> M ABA Bactoagar
101	+ v	-	3%	6.0	100 mg myo-inositol Bactoagar
142	+ v	-	6%	6.0	5 mg BAP 0.186 mg NAA 0.175 mg IAA 0.403 mg 2-IP 200 mg myo-inositol Bactoagar
163	+ v	-	3%	6.0	3.3 mg dicamba 100 mg myo-inositol Bactoagar
171	+ v	-	3%	6.0	0.25 mg 2,4-D 10 mg BAP 100 mg myo-inositol Bactoagar
173	+ v	-	6%	6.0	5 mg BAP 0.186 mg NAA 0.175 mg IAA 0.403 mg 2-IP 10 <sup>-5</sup> M ABA 200 mg myo-inositol Bactoagar
177	+ v	-	3%	6.0	0.25 mg 2,4-D 10 mg BAP 10 <sup>-5</sup> M ABA 100 mg myo-inositol Bactoagar
201	-	+	2%	5.8	25 mM proline

\* Basic MS medium described in reference 30. The medium described in ref. 30 is typically modified by decreasing the NH<sub>4</sub>NO<sub>3</sub> from 1.64 g/l to 1.55 g/l, and omitting the pyridoxine HCl, nicotinic acid, myoinositol and glycine.

+ = present; - = absent; v=vitamins

\*\* NAA = Napthol Acetic Acid

IAA = Indole Acetic Acid

2-IP = 2, isopentyl adenine

2,4-D = 2, 4-Dichlorophenoxyacetic Acid

BAP = 6-benzyl aminopurine

ABA = abscisic acid

Table 1: (continued)

Illustrative Embodiments of Tissue Culture Media Which are Used for Type II Callus Development, Development of Suspension Cultures and Regeneration of Maize Plant Cells					
Medium					
Id. Number	MS*	N6	Sucrose	Optimal pH	Other Components**
		v			1 mg 2,4-D 100 mg casein hydrolysate Gelgro <sup>R</sup>
205	-	+ v	2%	5.8	25 mM proline 0.5 mg 2,4-D 100 mg casein hydrolysate Gelgro <sup>R</sup>
227	-	+ v	2%	5.8	25 mM proline 13.2 mg dicamba 100 mg casein hydrolysate Gelgro <sup>R</sup>
401	+	-	3%	6.0	0.25 mg thiamine 1 mg 2,4-D 2 mg NAA 200 mg casein hydrolysate 500 mg K sulfate 100 mg myo-inositol 400 mg K phosphate (monobasic)
402	+	-	3%	6.0	0.25 mg thiamine 25 mM proline 1 mg 2,4-D 200 mg casein hydrolysate 500 mg K sulfate 400 mg K phosphate (monobasic) 100 mg myo-inositol

\* Basic MS medium described in reference 30. The medium described in ref. 30 is typically modified by decreasing the  $\text{NH}_4\text{NO}_3$  from 1.64 g/l to 1.55 g/l, and omitting the pyridoxine HCl, nicotinic acid, myoinositol and glycine.

+ = present; - = absent; v=vitamins

\*\* NAA = Napthol Acetic Acid

IAA = Indole Acetic Acid

2-IP = 2, isopentyl adenine

2,4-D = 2, 4-Dichlorophenoxyacetic Acid

BAP = 6-benzyl aminopurine

ABA = abscisic acid

Table 1: (continued)

Illustrative Embodiments of Tissue Culture Media Which are Used for Type II Callus Development, Development of Suspension Cultures and Regeneration of Maize Plant Cells					
Medium					
Id. Number	MS*	N6	Sucrose	Optimal pH	Other Components**
409	+	-	3%	6.0	0.25 mg thiamine 25 mM proline 10 mg dicamba 200 mg casein hydrolysate 500 mg K sulfate 400 mg K phosphate (monobasic) 100 mg myo-inositol
501	-	-	2%	5.7	Clark's *** Gelgro <sup>R</sup>

\* Basic MS medium described in reference 30. The medium described in ref. 30 is typically modified by decreasing the  $\text{NH}_4\text{NO}_3$  from 1.64 g/l to 1.55 g/l, and omitting the pyridoxine HCl, nicotinic acid, myoinositol and glycine.

+ = present; - = absent; v=vitamins

\*\* NAA = Naphthol Acetic Acid

IAA = Indole Acetic Acid

2-IP = 2, isopentyl adenine

2,4-D = 2, 4-Dichlorophenoxyacetic Acid

BAP = 6-benzyl aminopurine

ABA = abscisic acid

\*\*\* Basic medium described in reference 6

#### **Example 1: Initiation of the Suspension Culture Gil(A188XB73)716 (designated SC716) for Use in Transformation**

This Example describes the development of a maize suspension culture, designated SC716, which was employed in various of the transformation studies described hereinbelow. The Type II tissue used to initiate the cell suspension was derived from immature embryos of A188 x B73 plated onto N6-based medium with 1 mg/ml 2,4-D (201; see Table 1). A Type II callus was initiated by visual selection of fast growing, friable embryogenic cells. The suspension was initiated within 6 months after callus initiation. Tissue chosen from the callus to initiate the suspension consisted of very undifferentiated Type II callus, the characteristics of this undifferentiated tissue are the earliest stages of embryo development along with the soft, friable, undifferentiated tissue underlying it.

Approximately one gram of tissue was added to 20 mls of liquid medium. In this example, the liquid medium was medium 402 to which different slow-release hormone capsule treatments were added (see Example 12 below). These capsule treatments included 2,4-D, NAA, 2,4-D plus NAA, and 2 NAA capsules. One flask was initiated for each of the different 402 media plus hormone combinations. Every 7 days each culture was subcultured into fresh medium by transferring a small portion of the cellular suspension to a new flask. This involved swirling the original flask to suspend the cells (which tend to settle to the bottom of the culture vessel), tilting the flask on its side and allowing the denser cells and cell aggregates to settle slightly. One ml of packed cells was then drawn off from this pool of settled cells together with 4 mls of conditioned medium. A sterile ten ml, wide tip, pipet was used for this transfer (Falcon 7304). Any very large aggregates of cells which would not pass easily through the pipet tip were excluded. If a hormone capsule was present, it was also transferred to the new flask.

After approximately 7 weeks, the loose embryogenic cell aggregates began to predominate and fragment in each of the cultures, reaching a state referred to as "dispersed." The treatment which yielded the highest proportion of embryogenic clusters was the 402 medium plus a NAA capsule. After the cultures became dispersed and were growing at a fast rate, doubling approximately every two to three days as determined by increase in packed cell volume, a one ml packed cell inoculum from each culture was transferred into 401 medium using a ten ml narrow tip pipet (Falcon 7551). These transfers were performed about every 3½ days. An inoculum from the 402 plus 2,4-D plus NAA capsules culture was also used to initiate a culture in 409 medium (402 minus 2,4-D and plus 10mg/l dicamba) either with or

without 1 ml coconut water (Gibco 670-8130AG).

The most dispersed cultures were cryopreserved after 2 weeks, 2 months or 5 months.

The culture grown on 409 with coconut water was brought out of cryopreservation eight months later and thawed, cultured for two weeks on solid 201 culture medium using BMS as a feeder layer (38) and transferred to media 409 without coconut water. The culture was maintained by subculturing twice weekly, using 409 media, by the method described above.

#### **Example 2: Initiation of the Suspension Culture (A188 X B73)82 (designated SC82) for Use in Transformation**

This Example describes the development of another cell line employed in various of the transformation studies set forth below, termed SC82. In the development of SC82, inoculum for suspension culture initiation was visually selected from a Type II callus that was derived from immature embryos plated on a N6-based medium containing 13.2 mg/l dicamba (227) (Table 1). The suspension culture was initiated within 3 months of initiation of the Type II callus. Small amounts (50-100 mg) of callus distinguishable by visual inspection because of its highly proembryonic morphology, were isolated from more mature or organized structures and inoculated into a 50 ml flask containing 5 mls of filter-sterilized conditioned medium from the various GII (A188 x B73) 716 suspension cultures (402 medium with four types of capsule treatments and 409 medium).

After one week, this 5 ml culture was sieved through a 710 micron mesh and used to inoculate 20 mls of corresponding fresh and filter-sterilized conditioned medium from the established GII (A188 x B73) 716 cultures in 150 ml flasks. After one week or more of growth, two mls of packed cells were subcultured to fresh media by the method described above. The suspension culture maintained on 409 by this method was then cryopreserved within 3 months. The original cell line, which was maintained on 409 (not a reinoculated cryopreserved culture) was used in experiments 1 and 2 months later which resulted in stable transformation and selection (see Table 2 below). The cryopreserved culture was used for experiment 6 (see Table 2 below).

#### **C. Slow Release Plant Hormone Capsules**

Studies following the fate of radioactively labelled plant hormones (2,4-D and NAA) showed that within two days corn cells absorb most of the auxins present in suspension culture media. This problem of hormone depletion can be overcome by spiking the cultures with a small amount of auxin every other day. However, spiking cultures is very time consuming when done on a large scale and also increases the risk of contamination as the culture vessels must be opened frequently. Slow release plant hormone capsules were developed to overcome these problems. In summary, these capsules comprise a plant hormone, usually in a crystalline state, encapsulated in a silicone matrix surrounded by a silicone limiting membrane. The rate of hormone release is controlled by the size of the diffusible area and the thickness of the membrane. They have the advantages of 1) supplying hormones at an acceptable and predictable rate (e.g., 20 - 100 µg/20 ml culture media/day, 2) they are of a convenient size (e.g., 0.5 - 1.5 cm in length) for use in liquid or solid culture medium, 3) they are very durable and easily sterilized by autoclaving, and 4) they can be stored dry until needed.

The present formulation involves the controlled release of a plant hormone or selective agent for a plant tissue culture from an inner matrix containing crystals of the desired agent through an outer diffusion limiting membrane. A preferred embodiment of the formulation is to mix 30% dry crystals of the desired agent with 70% (w/w) room temperature vulcanizing (RTV) silicone which is then injected into silicone tubing having an appropriate diameter and wall thickness for the desired release rate of the desired agent. (The preferred agents for employing in connection with the slow release capsules are 2,4-D and NAA, and the preferred dimensions are 0.062" ID x 0.125" OD).

The RTV silicone is then polymerized at room temperature or at a higher temperature to accelerate the vulcanization process. Following vulcanization of the inner matrix, the tubing is cut to desired lengths and the ends sealed with RTV silicone. The preferred lengths for use in connection with the present invention are about 0.5 cm. After the end seals have polymerized, the resulting capsules can either be stored, as is, or autoclaved for 15 minutes on a fast exhaust cycle and stored indefinitely in a sterile form. Prior to use the capsules may be equilibrated to establish a stable diffusion gradient across the membrane, or used directly without equilibration.

Another formulation for a much lower release rate is to enclose crystals of a desired substance suspended in a liquid such as water or silicone oil in a relatively nonpermeable tubing such as Nylon-11. The release rate from this reservoir can then be regulated by drilling various size holes in the tubing and glueing a silicone window over the hole with silicone medical adhesive. Once again the capsules can be sterilized by autoclaving and stored dry until use.

An exemplary technique employed by the inventors for preparing slow release hormone capsules is as follows:

1. Two grams of Dow Corning MDX-4-4210 medical grade elastomer and 0.2 grams of Dow Corning MDX-4-4210 curing agent were weighed into a 10 ml syringe, the bottom of which was capped with a plastic cap.

2. Six-hundred mg of 2,4-D (or NAA), from which lumps have been removed by sieving through a 411 $\mu$  stainless steel sieve, was added to the same syringe and thoroughly mixed with the elastomer and curing agent.

3. The 10 ml syringe and its contents were then degassed for 1/2 hr in a vacuum centrifuge to remove bubbles.

4. Dow Corning Silastic medical grade silicone tubing (0.062" ID x 0.125" OD) of medium durometer (50 Shore A) was preswelled 10 to 30 minutes by soaking in acetone.

5. The plastic cap was removed from the end of the 10 ml syringe and the degassed silicone-2,4-D mixture was extruded into the preswollen tubing from which excess acetone had been removed by blowing a stream of air briefly through it.

6. Both ends of the filled tubing were then clamped shut and the tubing heated at 50 degrees (the boiling point of acetone = 56.5 degrees) overnight to accelerate the polymerization.

7. The tubing was then cut into 0.5 cm lengths.

8. The ends of the tubing sections were sealed with Dow Corning Type A medical adhesive and allowed to dry for 24 hr.

9. The finished capsules are autoclaved dry for 15-20 min and stored dry until use.

10. Before use the capsules may be preequilibrated for 48 hr by shaking in 25 ml of sterile 1 to 10 mM KHCO<sub>3</sub>, or added to cultures without equilibration.

#### **D. Cryopreservation Methods**

Cryopreservation is important because it allows one to maintain and preserve a cell culture for future use.

Cell suspensions were cryopreserved using modifications of methods previously reported (15,49). The cryopreservation protocol comprised adding a pre-cooled (0°C) concentrated cryoprotectant mixture dropwise over a period of one hour while stirring the cell suspension, which was also maintained at 0°C during this period. The volume of added cryoprotectant was equal to the initial volume of the cell suspension (1:1 addition), and the final concentration of cryoprotectant additives was 10% dimethyl sulfoxide, 10% polyethylene glycol (6000 MW), 0.23 M proline and 0.23 M glucose. The mixture was allowed to equilibrate at 0°C for 30 minutes, during which time the cell suspension/ cryoprotectant mixture was divided into 1.5 ml aliquot (0.5 ml packed cell volume) in 2 ml polyethylene cryo-vials. The tubes were cooled at 0.5°C/minute to -8°C and held at this temperature for ice nucleation.

Once extracellular ice formation had been visually confirmed, the tubes were cooled at 0.5°C/minute from -8 to -35°C. They were held at this temperature for 45 minutes (to insure uniform freeze-induced dehydration throughout the cell clusters). At this point, the cells had lost the majority of their osmotic volume (i.e. there is little free water left in the cells), and they could be safely plunged into liquid nitrogen for storage. The paucity of free water remaining in the cells in conjunction with the rapid cooling rates from -35 to -196°C prevented large organized ice crystals from forming in the cells. The cells are stored in liquid nitrogen, which effectively immobilizes the cells and slows metabolic processes to the point where long-term storage should not be detrimental.

Thawing of the extracellular solution was accomplished by removing the cryo-tube from liquid nitrogen and swirling it in sterile 42°C water for approximately 2 minutes. The tube was removed from the heat immediately after the last ice crystals had melted to prevent heating the tissue. The cell suspension (still in the cryoprotectant mixture) was pipetted onto a filter, resting on a layer of agarose-immobilized BMS cells (the feeder layer which provided a nurse effect during recovery). Dilution of the cryoprotectant occurred slowly as the solutes diffused away through the filter and nutrients diffused upward to the recovering cells. Once subsequent growth of the thawed cells was noted, the growing tissue was transferred to fresh culture medium. The cell clusters were transferred back into liquid suspension medium as soon as sufficient cell mass had been regained (usually within 1 to 2 weeks). After the culture was reestablished in liquid (within 1 to 2 additional weeks), it was used for transformation experiments. When necessary, previously cryopreserved cultures may be frozen again for storage.

#### **E. DNA Segments Comprising Exogenous Genes**

As mentioned previously, there are several methods to construct the DNA segments carrying DNA into a host cell that are well known to those skilled in the art. The general construct of the vectors used herein are plasmids comprising



a promoter, other regulatory regions, structural genes, and a 3' end.

DNA segments encoding the *bar* gene were constructed into a plasmid, termed pDPG165, which was used to introduce the bialaphos resistance gene into recipient cells (see Figures 1A and C). The *bar* gene was cloned from *Streptomyces hygroscopicus* (53) and exists as a 559-bp Sma I fragment in plasmid pIJ4101. The sequence of the coding region of this gene is identical to that published (45). To create plasmid pDPG165, the Sma I fragment from pIJ4104 was ligated into a pUC19-based vector containing the Cauliflower Mosaic Virus (CaMV) 35S promoter (derived from pBI221.1, provided by R. Jefferson, Plant Breeding Institute, Cambridge, England), a polylinker, and the transcript 7 (Tr7) 3' end from *Agrobacterium tumefaciens* (3' end provided by D. Stalker, Calgene, Inc., Davis, CA).

An additional vector encoding GUS, pDPG208, (Figures 1B and D) was used in these experiments. It was constructed using a 2.1 kb BamHI/EcoRI fragment from pAGUS1 (provided by J. Skuzeski, University of Utah, Salt Lake City, UT) containing the coding sequence for GUS and the *nos* 3'-end from *Agrobacterium tumefaciens*. In pAGUS1 the 5'-noncoding and 5'-coding sequences for GUS were modified to incorporate the Kozak consensus sequence (24) and to introduce a new HindIII restriction site 6 bp into the coding region of the gene (see Figure 1E). The 2.1 kb BamHI/EcoRI fragment from pAGUS1 was ligated into a 3.6 kb BamHI/EcoRI fragment of a pUC19-based vector pCEVI (provided by Calgene, Inc., Davis, CA). The 3.6 kb fragment from pCEVI contains pUC19 and a 430 bp 35S promoter from cauliflower mosaic virus adjacent to the first intron from maize *Adh1*.

In terms of an R gene complex for use in connection with the present invention, the most preferred vectors contain the 35S promoter from Cauliflower mosaic virus, the first intron from maize *Adh1*, the Kozak consensus sequence, Sn:bol3 cDNA, and the transcript 7 3' end from *Agrobacterium tumefaciens*. One such vector prepared by the inventors is termed pDPG237. To prepare pDPG237 (see Figure 1F), the cDNA clone of Sn:bol3 was obtained from S. Dellaporta (Yale University, USA). A genomic clone of Sn was isolated from genomic DNA of Sn:bol3 which had been digested to completion with HindIII, ligated to lambda arms and packaged in vitro. Plaques hybridizing to two regions of cloned R alleles, R-nj and R-sc (54) were analyzed by restriction digest. A 2 kb Sst-HincII fragment from the pSn7.0 was used to screen a cDNA library established in lambda from RNA of light-irradiated scutellar nodes of Sn:bol3. The sequence and a restriction map of the cDNA clone was established.

The cDNA clone was inserted into the same plant expression vector described for pDPG165, the *bar* expression vector (see above), and contains the 35S Cauliflower mosaic virus promoter, a polylinker and the transcript 7 3' end from *Agrobacterium tumefaciens*. This plasmid, pDPG232, was made by inserting the cDNA clone into the polylinker region; a restriction map of pDPG232 is shown in Figure 1G. The preferred vector, pDPG237, was made by removing the cDNA clone and Tr7 3' end from pDPG232, with Aval and EcoRI and ligating it with a BamHI/EcoRI fragment from pDPG208. The ligation was done in the presence of a BamHI linker as follows:

**GATCCGTCGACCATGGCGCTTCAAGCTTC**  
**GCAGCTGGTACCGCGAAGTTCTGAAGGGCT**

The final construct of pDPG237 contained a Cauliflower mosaic virus 35S promoter, the first intron of *Adh1*, Kozak consensus sequence, the BamHI linker, cDNA of Sn:bol3, and the Tr7 3' end and is shown in Figure 1F.

Additional vectors have been prepared using standard genetic engineering techniques. For example, a vector, designated pDPG128, has been constructed to include the *neo* coding sequence (neomycin phosphotransferase (APH (3')-II)). Plasmid pDPG128 contains the 35S promoter from CaMV, the neomycin phosphotransferase gene from Tn5 (66) and the Tr7 terminator from *Agrobacterium tumefaciens*. Another vector, pDPG154, incorporates the crystal toxin gene and was also prepared by standard techniques. Plasmid pDPG154 contains the 35S promoter, the entire coding region of the crystal toxin protein of *Bacillus thuringiensis* var. *kurstaki* HD 263, and the Tr7 promoter.

Various tandem vectors have also been prepared. For example, a *bar/aroA* tandem vector was constructed by ligating a blunt-ended 3.2 kb DNA fragment containing a mutant EPSP synthase *aroA* expression unit (64) to NdeI-cut pDPG165 that had been blunted and dephosphorylated (NdeI introduces a unique restriction cut approximately 200 bp downstream of the Tr7 3'-end of the *bar* expression unit). Transformants having *aroA* in both orientations relative to *bar* were identified.

#### **F. Methods of Delivering DNA to Cells**

A DNA delivery system that does not require protoplast isolation or introduction of *Agrobacterium* DNA is microprojectile bombardment (8,23). There are several potential cellular targets for microprojectile bombardment to produce fertile transgenic plants: pollen, microspores, meristems, and cultured embryogenic cells are but a few examples. Germ-line transformation in maize has not been previously reported by bombardment of any of these types.

One of the newly emerging techniques for the introduction of exogenous DNA constructs into plant cells involves

the use of microprojectile bombardment. The details of this technique and its use to introduce exogenous DNA into various plant cells are discussed in Klein, 1989, Wang, et al., 1988 and Christou, et al., 1988 (22,50,8). One method of determining the efficiency of DNA delivery into the cells via microprojectile bombardment employs detection of transient expression of the enzyme  $\beta$ -glucuronidase (GUS) in bombarded cells. For this method, plant cells are bombarded with a DNA construct which directs the synthesis of the GUS enzyme.

Apparati are available which perform microprojectile bombardment. A commercially available source is an apparatus made by Biolistics, Inc. (now DuPont), but other microprojectile or acceleration methods are within the scope of this invention. Of course, other "gene guns" may be used to introduce DNA into cells.

Several modifications of the microprojectile bombardment method were made by the inventors. For example, stainless steel mesh screens were introduced below the stop plate of the bombardment apparatus, i.e., between the gun and the cells. Furthermore, modifications to existing techniques were developed by the inventors for precipitating DNA onto the microprojectiles.

### Example 3: Microprojectile Bombardment

For bombardment, friable, embryogenic Type-II callus (1) was initiated from immature embryos essentially as set forth above in Examples 1 and 2. The callus was initiated and maintained on N6 medium (5) containing 2 mg/l glycine, 2.9 g/l L-proline, 100 mg/l casein hydrolysate, 13.2 mg/l dicamba or 1 mg/l 2,4-D, 20 g/l sucrose, pH 5.8, solidified with 2 g/l Gelgro (ICN Biochemicals). Suspension cultures initiated from these callus cultures were used for bombardment.

In the case of SC82, suspension culture SC82 was initiated from Type-II callus maintained in culture for 3 months. SC82 cells (see Example 1) were grown in liquid medium for approximately 4 months prior to bombardment (see Table 2, experiments #1 and #2). SC82 cells were also cryopreserved 5 months after suspension culture initiation, stored frozen for 5 months, thawed and used for bombardment (experiment #6).

In the case of suspension culture SC716 (see Example 2), it was initiated from Type-II callus maintained 5 months in culture. SC716 cells were cultured in liquid medium for 5 months, cryopreserved for 8 months, thawed, and used two months later in bombardment experiments #4 and #5. SC94 was initiated from 10 month old Type-II callus; and cultured in liquid medium for 5 months prior to bombardment (experiment #3).

Prior to bombardment, recently subcultured suspension culture cells were sieved through 1000  $\mu$ m stainless steel mesh. From the fraction of cell clusters passing through the sieve, approximately 0.5 ml packed cell volume (PCV) was pipetted onto 5 cm filters (Whatman #4) and vacuum-filtered in a Buchner funnel. The filters were transferred to petri dishes containing three 7 cm filters (Whatman #4) moistened with 2.5 ml suspension culture medium.

The dish containing the filters with the immobilized cell suspensions was positioned 6 cm below the lexan plate used to stop the nylon macroprojectile. With respect to the DNA, when more than a single plasmid was used, plasmid DNA was precipitated in an equimolar ratio onto tungsten particles (average diameter approximately 1.2  $\mu$ m, GTE Sylvania) using a modification of the protocol described by Klein, et al. (1987). In the modified procedure, tungsten was incubated in ethanol at 65 degrees C. for 12 hours prior to being used for precipitation. The precipitation mixture included 1.25 mg tungsten particles, 25  $\mu$ g plasmid DNA, 1.1 M  $\text{CaCl}_2$  and 8.7 mM spermidine in a total volume of 575  $\mu$ l. After adding the components, in the above order, the mixture was vortexed at 4° C for 10 min, centrifuged (500 X G) for 5 min and 550  $\mu$ l of supernatant was decanted. From the remaining 25  $\mu$ l of suspension, 1  $\mu$ l aliquots were pipetted onto the macroprojectile for bombardment.

Each plate of suspension cells was bombarded twice at a vacuum of 28 inches Hg. In bombarding the embryogenic suspensions of A188 X B73 and A188 X B84, 100  $\mu$ m or 1000  $\mu$ m stainless steel screens were placed about 2.5 cm below the stop plate in order to increase the number of foci while decreasing their size and also to ameliorate injury to the bombarded tissue. After bombardment, the suspension cells and the supporting filter were transferred onto solid medium or the cells were scraped from the filter and resuspended in liquid culture medium.

Cells from embryogenic suspension cultures of maize were bombarded with the bar-containing plasmid pDPG165 alone or in combination with a plasmid encoding GUS, pDPG208 (Fig. 1). In experiments in which a GUS plasmid was included, two of the filters containing bombarded cells were histochemically stained 48h post-bombardment. The total number of foci (clusters of cells) per filter transiently expressing GUS was at least 1000. In two separate studies designed to quantitate transiently expressing cells (using an SC82 (A188 x B73) suspension culture), the mean number and standard deviation of GUS-staining foci per filter was 1472  $\pm$  211 and 2930  $\pm$  (n=3 and 4, respectively). The number of cells in individual foci that expressed GUS averaged 2-3 (range 1-10). Although histochemical staining can be used to detect cells transformed with the gene encoding GUS, those cells will no longer grow and divide after staining. For detecting stable transformants and growing them further, e.g., into plants, selective systems compatible with viability are required.

### G. Methods of Identifying Transformed Cells

It is believed that DNA is introduced into only a small percentage of cells in any one experiment. In order to provide a more efficient system for identification of those cells receiving DNA and integrating it into their genomes, therefore, one may desire to employ a means for selecting those cells that are stably transformed. One exemplary embodiment of such a method is to introduce into the host cell, a marker gene which confers resistance to some agent, e.g. an antibiotic or herbicide. The potentially transformed cells are then exposed to the agent. In the population of surviving cells are those cells wherein generally the resistance-conferring gene has been integrated and expressed at sufficient levels to survive. Cells may be tested further to confirm stable integration of the exogenous DNA. Using embryogenic suspension cultures, stable transformants are recovered at a frequency of approximately 1 per 1000 transiently expressing foci. A specific embodiment of this procedure is shown in Example 5.

One of the difficulties in corn transformation, has been the lack of an effective selective agent for transformed cells, from totipotent cultures (36). Stable transformants were recovered from bombarded nonembryogenic Black Mexican Sweet (BMS) maize suspension culture cells, using the neo gene and selection with the aminoglycoside, kanamycin (22). This approach is limited because many monocots are insensitive to high concentrations of aminoglycosides (12,19). The stage of cell growth, duration of exposure and concentration of the antibiotic, may be critical to the successful use of aminoglycosides as selective agents to identify transformants (26,51,52). In addition, use of the aminoglycosides, kanamycin or G418, to select stable transformants from embryogenic maize cultures, in the inventors' experience, often results in the isolation of resistant calli that do not contain the *neo* gene.

One herbicide which has been suggested in resistance studies is the broad spectrum herbicide bialaphos. Bialaphos is a tripeptide antibiotic produced by *Streptomyces hygroscopicus* and is composed of phosphinothricin (PPT), an analogue of L-glutamic acid, and two L-alanine residues. Upon removal of the L-alanine residues by intracellular peptidases, the PPT is released and is a potent inhibitor of glutamine synthetase (GS), a pivotal enzyme involved in ammonia assimilation and nitrogen metabolism (33). Inhibition of GS in plants by PPT causes the rapid accumulation of ammonia and death of the plant cells.

The organism producing bialaphos also synthesizes an enzyme phosphinothricin acetyl transferase (PAT) which is encoded by the *bar* gene. The use of the herbicide resistance gene encoding phosphinothricin acetyl transferase (PAT) is referred to in DE 3642 829 A wherein the gene is isolated from *Streptomyces viridochromogenes*. This enzyme acetylates the free amino group of PPT preventing auto-toxicity (45). The *bar* gene has been cloned (29,45) and expressed in transgenic tobacco, tomato and potato plants (10) and *Brassica* (11). In previous reports, some transgenic plants which expressed the resistance gene were completely resistant to commercial PPT and bialaphos in greenhouses.

PCT Application No. WO 87/00141 refers to the use of a process for protecting plant cells and plants against the action of glutamine synthetase inhibitors. This application also refers to the use of such of a process to develop herbicide resistance in determined plants. The gene encoding resistance to the herbicide BASTA (Hoechst phosphinothricin) or Herbiace (Meiji Seika bialaphos) was said to be introduced by *Agrobacterium* infection into tobacco (*Nicotiana tabacum* cv Petit Havan SR1), potato (*Solanum tuberosum* cv Benolima) and tomato (*Lycopersicum esculentum*) and conferred on plants resistance to application of herbicides.

An exemplary embodiment of vectors capable of delivering DNA to plant host cells is the plasmid, pDPG165. This plasmid is illustrated in Fig. 1A and 1C. A very important component of this plasmid for purposes of genetic transformation is the *bar* gene which acts as a marker for selection of transformed cells.

#### Example 4: Selection of *bar* Transformants Using Bialaphos

The suspension culture (designated SC82) used in the initial experiments (see Example 3) was derived from embryogenic Type-II callus of A188 X B73. Following bombardment (see Example 3), cells on filters were resuspended in nonselective liquid medium, cultured for 1 to 2 weeks and transferred to filters overlaying solid medium containing 1 or 3 mg/l bialaphos. The degree of inhibition of tissue growth during selection was dependent upon the density of the cells on the filter and on the concentration of bialaphos used. At the density plated (0.5 PCV/filter), the growth of the cells cultured on 1 mg/l bialaphos was only partially inhibited (~30-50% of nonselected growth) and after 3 to 4 weeks much of this tissue was transferred as discrete clumps (~5 mm in diameter) to identical medium. On medium containing 3 mg/l bialaphos, the growth of cells on the original selection filter was severely inhibited (~10% of nonselected growth) and selection was carried out without removing the tissue from the original filter.

Using either selection protocol (1 or 3 mg/l bialaphos), resistant cell colonies emerged on the selection plates of SC82 bombarded with pDPG165 approximately 6 to 7 weeks after bombardment (Fig. 2A). Bialaphos-resistant calli were maintained and expanded on selection medium. Much of this tissue was embryogenic (Fig. 2B). No colony growth occurred on plates to which cells were added from suspension cultures on which no transforming attempts were made. These are controls which confirm the prediction that cells without the *bar* gene are not resistant to bialaphos.

Colonies on solid supports are visible groups of cells formed by growth and division of cells plated on such support. Colonies can be seen in Fig. 2A on a petri dish. In this figure, the cells capable of growth are those that are resistant to the presence of the herbicide bialaphos, said resistance resulting from integration and expression of the *bar* gene. Exposure of cells was to 1 mg/l bialaphos. Figure 2B is a magnification showing the morphology of one bialaphos-resistant culture maintained on selection media indicating that growth is embryogenic.

As a confirmation that the cells forming the colonies shown in Fig. 2 had indeed incorporated the *bar* gene and were expressing it, bialaphos-resistant callus lines were analyzed for activity of the *bar* gene product, phosphinothricin acetyl transferase (PAT), by thin-layer chromatography. Protein extracts from eleven callus lines (E1-11) isolated from SC82 bombardment experiments contained PAT activity as shown in Figure 3 and activity levels varied approximately 10-fold among the isolates.

Still further and more direct confirmation of the presence of the *bar* gene was obtained by analysis of the genomic DNA of potential transformants by DNA gel blots (Figure 4). The sources of DNA which were electrophoresed through the gel were the bialaphos-resistant callus lines designated E1-E11 and a non-selected control, EO. (Fig. 1 indicates the cleavage sites of those enzymes within the *bar* gene plasmid.) After the DNA was electrophoresed through the gel and transferred to nylon membranes, the resulting blot was hybridized with a <sup>32</sup>P-labeled *bar* gene sequence from the plasmid pDPG165. The radioactivity used per blot was approximately 25 X 10<sup>6</sup> Cerenkov cpm. The lane in Figure 4 designated "1" and "5" copies contain 1.9 and 9.5 pg respectively of the 1.9 kb *bar* expression unit released from the plasmid pDPG165 by application of the EcoRI and HindIII enzymes; these amounts represent about 1 and 5 copies per diploid genome.

Genomic DNA from all eleven bialaphos-resistant isolates contained *bar*-hybridizing sequences as shown in Figure 4. The hybridization in all isolates to a fragment migrating slightly larger than 2 kb may be due to contaminating pUC19 sequences contained in this *bar* probe preparation; no such hybridization occurred in subsequent experiments using the same genomic DNA and a different preparation of the *bar* probe. Hybridization to a 1.9 kb fragment in eight of the eleven isolates indicated that these isolates contained intact copies of the 1.9 kb *bar* expression unit. The estimated copy numbers of the intact unit ranged from one or two (E1, E7, E8, E10, E11) to approximately 20 (E3, E4, E6). Hybridization with the *bar* probe in isolates E2 and E5 occurred only to a single, higher molecular weight fragment (~3 kb).

To establish that the PAT coding sequence was intact in isolates E2 and E5, genomic DNA was digested with SmaI, which releases a 559 bp fragment containing the PAT structural gene (Figure 1A), and subjected to DNA gel blot analysis using <sup>32</sup>P-labeled *bar*. This analysis confirmed the presence of a single intact copy of *bar*. Expression of PAT in these isolates may not be dependent on the 35S promoter or the Tr7 3' end. The hybridization patterns of some of the isolates were identical (E2 and E5; E7 and E8; E3, E4, and E6); therefore, it is probable that some isolates did not arise from independent transformation events but represent transformants that were separated during selection.

Seven hybridization patterns were unique, likely representing seven independent single-cell transformation events. The patterns and intensities of hybridization for the seven transformants were unchanged during four months in culture, providing evidence for the stability of the integrated sequences. The seven independent transformants were derived from two separate bombardment experiments. Four independent transformants representing isolates E2/E5, E3/E4/E6, E1 and E7/E8, were recovered from a total of four original filters from bombardment experiment #1 and the three additional independent transformants, E9, E10, and E11, were selected from tissue originating from six bombarded filters in experiment #2. These data are summarized in Table 2.

Table 2  
Summary of Maize Transformation Experiments

Exp. #	Culture Bombarded	# of Filters Bombarded	# of Independent bar Transforms Recovered	# with Intact bar Expression Units	# with GUS Coding Sequence	# with GUS Activity	Cointegration Frequency (%)	Coexpression Frequency (%)
1	SC82	4	4	3	n.a.			
2	SC82	6	3	2	n.a.			
3	SC94	10	8	6	n.a.			
4	SC716*	8	13	8	11	3	85	23
5	SC716*	8	7	4	6	1	86	14
6	SC82*	4	19	17	13	3	68	16
Totals		40	54	40	30	7	77(30/39)	18(7/39)

\* culture reinitiated from cryopreserved cells

n.a. not applicable; only pDPG165 DNA used or cotransformation analysis not done

Studies with other embryogenic suspension cultures produced similar results. Using either an SC82 culture that was reinitiated from cryopreserved cells (experiment #6) or an A188 x B84 (SC94) suspension culture (experiment #3), numerous independent transformants were recovered (19 and 18 respectively; Table 2). All transformants contained the *bar* gene and expressed PAT. The copy number of *bar*-hybridizing sequences and levels of PAT expression were comparable to the studies described above.

#### Example 5: Integration of the Bar Gene into Cell Lines Derived from the SC716 Suspension Culture

Bombardment studies and subsequent analyses were also performed on the A188xB73 suspension culture, termed SC716 (see Example 1). The resultant transformed plant cells were analyzed for integration of *bar* genes. To carry out this analysis, genomic DNA was obtained from R1-R21 isolates; 6 µg of DNA was digested with the restriction endonucleases EcoRI and HindIII, and DNA gel blot analysis was performed using the *bar* gene as probe. In Fig. 9, molecular weights in kb are shown to the right and left. The untransformed control is designated "RO," and the last column to the right contains the equivalent of two copies of the *bar* gene expression unit per diploid genome. For the DNA load used, two copies the *bar* expression unit per diploid genome is 5.7 pg of the 1.9 kb EcoII/Hind fragment from the plasmid pDPG165. The DNA separated on the gel blot was hybridized to a <sup>32</sup>P-labeled *bar* probe. The label activity in the hybridization was approximately 10 X 10<sup>6</sup> Cerenkov cpm. In A, the presence of an intact *bar* expression unit is inferred from the hybridization of the *bar* probe to a 1.9 kb band in the gel.

#### Example 6: Assays for Integration and Expression of GUS

SC716 transformants discussed in Example 5, were further analyzed for integration and expression of the gene encoding GUS. As determined by histochemical assay, four of the SC716 transformants (R5, R7, R16, and R21) had detectable GUS activity 3 months post-bombardment. Expression patterns observed in the four coexpressing callus lines varied. The number of cells with GUS activity within any given transformant sampled ranged from ~5% to ~90% and, in addition, the level of GUS activity within those cells varied. The cointegration frequency was determined by washing the genomic blot hybridized with *bar* (Figure 9A) and probing with <sup>32</sup>P-labeled GUS sequence as shown in Figure 9B. EcoRI and HindIII, which excise the *bar* expression unit from pDPG165, also release from pDPG208 a 2.1 kb fragment containing the GUS coding sequence and the *nos* 3' end (Figure 1B).

Seventeen of the independent *bar* transformants contained sequences that hybridized to the GUS probe; three, R2, R14 and R19 did not. Transformants in which GUS activity was detected (R5, R7, R16 and R21) had intact copies of the 2.1 kb EcoRI/HindIII fragment containing the GUS structural gene (Figure 9B). Transformants that contained large numbers of fragments that hybridized to *bar* (R1, R5, R21) also contained comparable number of fragments that hybridized to the gene encoding GUS (Figures 9A and B). This observation is consistent with those reported using independent plasmids in PEG-mediated transformation of A188 X BMS protoplasts (Lyznik, et al., 1989) and in studies conducted by the inventors involving bombardment-mediated transformation of BMS suspension cells.

#### H. Co-Transformation

Co-transformation may be achieved using a vector containing the marker and another gene or genes of interest. Alternatively, different vectors, e.g., plasmids, may contain the different genes of interest, and the plasmids may be concurrently delivered to the recipient cells. Using this method, the assumption is made that a certain percentage of cells in which the marker has been introduced, have also received the other gene(s) of interest. As can be seen in the following examples, not all cells selected by means of the marker, will express the other genes of interest which had been presented to the cells concurrently. For instance, in Example 7, successful cotransformation occurred in 17/20 independent transformants (see Table 2), coexpression occurred in 4/20. In some transformants, there was variable expression among transformed cells.

#### Example 7: Co-Integration and Co-Expression of the Bar Gene and the GUS Gene to Cell Lines Derived from the SC82 Suspension Culture

Of the bialaphos-resistant isolates selected from a reinitiation of cryopreserved SC82 cells transformed with separate plasmids (as described for SC716), nineteen independent transformants were selected in this experiment (experiment #6, Table 2). The frequency of cointegration and coexpression in those isolates was similar to that described for SC716 isolates (Table 2). The pattern of GUS staining in these transformants varied in a manner similar to that described for coexpressing SC716 transformants. A transformant, Y13, which contained intact GUS coding sequence, exhibited varying levels of GUS activity as shown in Figure 8. This type of expression pattern has been described previously in cotransformed BMS cells (Klein, et al., 1989). Variable activity detected in the cells from a single trans-

formant may be attributed to unequal penetration of the GUS substrate, or differential expression, methylation, or the absence of the gene in some cells.

These results show that both the *bar* gene and the GUS gene are present in some of the cells bombarded with the two plasmids containing these genes. Co-transformation has occurred. In the cotransformation examples described herein and summarized in Table 2, cotransformation frequency of the non-selected gene was 77%; coexpression frequency was 18%.

### **I. Regeneration of Plants From Transformed Cells**

For use in agriculture, transformation of cells *in vitro* is only one step toward commercial utilization of these new methods. Plants must be regenerated from the transformed cells, and the regenerated plants must be developed into full plants capable of growing crops in open fields. For this purpose, fertile corn plants are required. The invention disclosed herein is the first successful production of fertile maize plants (e.g., see Figure 11A) from transformed cells.

One efficient regeneration system involves transfer of embryogenic callus to MS (Murashige and Skoog, 1962) medium containing 0.25 mg/l 2,4-dichlorophenoxyacetic acid and 10.0 mg/l 6-benzyl-aminopurine. Tissue was maintained on this medium for approximately 2 weeks and subsequently transferred to MS medium without hormones (Shillito, et al., 1989). Shoots that developed after 2-4 weeks on hormone-free medium were transferred to MS medium containing 1% sucrose and solidified with 2 g/l Gelgro<sup>R</sup> in Plant Con<sup>R</sup> containers where rooting occurred.

Another successful regeneration scheme involved transfer of embryogenic callus to N6 (Chu, et al., 1975) medium containing 6% sucrose and no hormones (Armstrong and Green, 1985) for two weeks followed by transfer to MS medium without hormones as described above. Regeneration was performed at 25°C under fluorescent lights (250 microeinsteins·m<sup>-2</sup>·s<sup>-1</sup>). After approximately 2 weeks developing plantlets were transferred to soil, hardened off in a growth chamber (85% relative humidity, 600 ppm CO<sub>2</sub>, 250 microeinsteins·m<sup>-2</sup>·s<sup>-1</sup>), and grown to maturity either in a growth chamber or the greenhouse.

Regeneration of plants from transformed cells requires careful attention to details of tissue culture techniques. One of the major factors is the choice of tissue culture media. There are many media which will support growth of plant cells in suspension cultures, but some media give better growth than others at different stages of development. Moreover, different cell lines respond to specific media in different ways. A further complication is that treatment of cells from callus initiation through transformation and ultimately to the greenhouse as plants, requires a multivariate approach. A progression consisting of various media types, representing sequential use of different media, is needed to optimize the proportion of transformed plants that result from each cell line. Table 3 illustrates sequential application of combinations of tissue culture media to cells at different stages of development. Successful progress is ascertained by the total number of plants regenerated.

## REGENERATION MEDIA PROGRESSIONS

X = Regeneration not attempted by this route.  
\* = More plants could have been taken to soil.

55



A preferred embodiment for use on cell lines in general, at least initially, is the combination shown in the second column under the regeneration media progression (media 227, 171, 101, 501). Media 227 is a good media for the selective part of the experiments, for example, to use for growth of callus in the presence of bialaphos. This media contains the hormone dicamba. NAA and 2,4-D are hormones in other media. In liquid media, these are usually encapsulated for controlled release (see Example 12 hereinbelow).

Thus, it can be seen from Table 1 that the various media are modified so as to make them particularly applicable to the development of the transformed plant at the various stages of the transformation process. For example, subculture of cells in media 171 after applying the selective agent, yields very small embryos. Moreover, it is believed that the presence of BAP in the media facilitates development of shoots. Myo-inositol is believed to be useful in cell wall synthesis. Shoot elongation and root development proceeds after transfer to media 101. 101 and 501 do not contain the hormones that are required for earlier stages of regeneration.

Transfer of regenerating plants is preferably completed in an agar-solidified media adapted from a nutrient solution developed by Clark (1982; ref. 6), media 501. The composition of this media facilitates the hardening of the developing plants so that they can be transferred to the greenhouse for final growth as a plant. The salt concentration of this media is significantly different from that of the three media used in the earlier stages, forcing the plant to develop its own metabolic pathways. These steps toward independent growth are required before plants can be transferred from tissue culture vessels (e.g. petri dishes, plant cans) to the greenhouse.

Approximately 50% of transformed callus lines derived from the initial SC82 and SC716 experiments were regenerable by the routes tested. Transgenic plants were regenerated from four of seven independent SC82 transformants and ten of twenty independent SC716 transformants.

Regeneration of thirteen independently, transformed cell lines and two control lines of SC716 was pursued. Regeneration was successful from ten of thirteen transformants. Although a total of 458 plantlets were regenerated, due to time and space constraints only 219 transformed plants (representing approximately 48% of the total number of regenerants) were transferred to a soilless mix (see below). Approximately 185 plants survived. Twelve regeneration protocols were investigated and the number of plants regenerated from each route has been quantified (Table 3). There appeared to be no significant advantage to maturing the tissues on 201, 52, 163, or 205 (see Table 1 for media codes) prior to transfer to medium 171 or 173. The majority of the plants were generated by subculturing embryogenic callus directly from 227 to either 171 or 173. These plantlets developed roots without addition of exogenous auxins, and plantlets were then transferred to a soilless mix, as was necessary for many of the transformants regenerated from SC82.

The soilless mix employed comprised Pro Mix, Micromax, Osmocote 14-14-14 and vermiculite. Pro Mix is a commercial product used to increase fertility and porosity as well as reduce the weight of the mixture. This is the bulk material in the mixture. Osmocote is another commercial product that is a slow release fertilizer with a nitrogen-phosphorus-potassium ratio of 14:14:14. Micromax is another commercial fertilizer that contains all of the essential micronutrients. The ratio used to prepare the soilless mix was: 3 bales (3 ft<sup>3</sup> each) Pro Mix; 10 gallons (vol.) vermiculite; 7 pounds Osmocote; 46 ml Micromax. The soilless mix may be supplemented with one or two applications of soluble Fe to reduce interveinal chlorosis during early seedling and plant growth.

Regeneration of transformed SC82 selected cell lines yielded 76 plants transferred to the soilless mix, and 73 survived. The plants were regenerated from six bialaphos-resistant isolates, representing four of seven clonally independent transformants. Eighteen protocols were used successfully to regenerate the seventy six plants (Table 4). Differences in morphology between cell lines deemed some protocols more suitable than others for regeneration.

## TABLE 4

[illegible]

• = See table 1 for media codes.  
X = This media progression was either attempted and unsuccessful or not attempted.

227A = 227 with  $10^{-7}$  M ABA.  
227B = 227 with 1 mg/1 blalaphos.

Prior to regeneration, the callus was transferred to either a) an N6-based medium containing either dicamba or 2,4-D or b) an MS-based medium containing 2,4-D. These steps allowed further embryoid development prior to maturation. Most of the maturation media contained high BAP levels (5-10mg/l) to enhance shoot development and cause proliferation. An MS-based medium with low 2,4-D (0.25 mg/l) and high BAP (10 mg/l), as described by Shillito, et al., 1989, was found to be quite effective for regeneration.

Likewise, an MS-based medium containing 1  $\mu$ m NAA, 1  $\mu$ m IAA, 2  $\mu$ m 2-IP, and 5 mg/l BAP (modified from Congar, et al., 1987) also promoted plant regeneration of these transformants. After plantlets recovered by any of the regenerative protocols had grown to five cm, they were transferred to a nutrient solution described by Clark, 1982, which was solidified with Gelgro. Plantlets which were slow to develop roots were treated with 3  $\mu$ l droplets of 0.3% IBA at the base of the shoot to stimulate rooting. Plants with well developed root systems were transferred to a soilless mix and grown in controlled environmental chambers from 5-10 days, prior to transfer to the greenhouse.

#### J. Assays for Integration of Exogenous DNA and Expression of DNA in $R_0$ $R_1$ Plants

Studies were undertaken to determine the expression of the transformed gene(s) in transgenic  $R_0$  and  $R_1$  plants. Functional activity of PAT was assessed by localized application of a commercial herbicide formulation containing PPT to leaves of SC82  $R_0$  and  $R_1$  plants. No necrosis was observed on leaves of  $R_0$  plants containing either high levels (E2/E5), or low levels (E3/E4) of PAT. Herbicide-treated E3/E4/E6 and control leaves are shown in Figure 10A. Herbicide was also applied to leaves of E2/E5 progeny segregating for *bar*. As demonstrated in Figure 10B, leaves of  $R_1$  plants expressing *bar* exhibited no necrosis six days after application of the herbicide while  $R_1$  plants without *bar* developed necrotic lesions. No necrosis was observed on transformed leaves up to 30 days post-application.

Twenty-one  $R_0$  plants, representing each of the four regenerable transformed SC82 callus lines, were also analyzed for expression of the *bar* gene product, PAT, by thin-layer chromatographic techniques. Protein extracts from the leaves of the plants were tested. PAT activity of one plant regenerated from each callus line is shown in Fig. 5.

All 21 plants tested contained PAT activity. Furthermore, activity levels were comparable to levels in the callus lines from which the plants were regenerated. The nontransformed plant showed no PAT activity (no band is in the expected position for acetylated PPT in the autoradiograph from the PAT chromatogram). A band appears in the BMS lane that is not in lanes containing protein extracts from the plant leaves. This extra band was believed to be an artifact.

As another method of confirming that genes had been delivered to cells and integrated, genomic (chromosomal) DNA was isolated from a nontransformed plant, the four regenerable callus lines and from two  $R_0$  plants derived from each callus line. Figure 6 illustrates results of gel blot analysis of genomic DNA from the four transformed calli (C) and the  $R_0$  plants derived from them. The transformed callus and all plants regenerated from transformed callus contained sequences that hybridized to the *bar* probe, indicating the presence of DNA sequences that were complementary to *bar*. Furthermore, in all instances, hybridization patterns observed in plant DNA were identical in pattern and intensity to the hybridization profiles of the corresponding callus DNA.

DNA from E3/E4/E6 callus and the desired  $R_0$  plants contained approximately twenty intact copies of the 1.9 kb *bar* expression unit (Cauliflower Mosaic Virus 35S promoter-*bar*-*Agrobacterium* transcript 7' 3'-end) as well as numerous other *bar*-hybridizing fragments. E11 callus and plant DNA contained 1-2 copies of the intact expression unit and 5-6 additional non-intact hybridizing fragments. E10 callus and plants contained 1-2 copies of the intact *bar* expression unit. E2/E5 DNA contained a single fragment of approximately 3 kb that hybridized to the probe. To confirm that the hybridizing sequence observed in all plants were integrated into the chromosomal DNA, undigested genomic DNA from one plant derived from each independent transformant was analyzed by DNA gel blot hybridization. Hybridization to *bar* was observed only in high molecular weight DNA providing evidence for the integration of *bar* into the maize genome.

Plants were regenerated from the coexpressing callus line, Y13, shown in Figure 8. Plants regenerated from Y13 (experiment #6, Table 2) were assayed for GUS activity and histochemically stained leaf tissue from one plant is shown in Figures 10C, D, E. Numerous cell types including epidermal, guard, mesophyll and bundle sheath cells stained positive for GUS activity. Staining intensity was greatest in the vascular bundles. Although all leaf samples from the regenerated plants tested (5/5) expressed the nonselected gene, some non-expressing leaf sectors were also observed. Leaf tissue extracts from three Y13 and three control plants were also assayed for GUS activity by fluorometric analysis (Jefferson, 1987). Activity detected in two opposing leaves from each of three Y13 plants tested was at least 100-fold higher than that in control leaves.

#### Example 8: General Methods for Assays

A method to detect the presence of phosphinothricin acetyl transferase (PAT) activity is to use thin layer chromatography.

An example of such detection is shown in Fig. 5 wherein various protein extracts prepared from homogenates of

potentially transformed cells, and from control cells that have neither been transformed nor exposed to bialaphos selection, are assayed by incubation with PPT and  $^{14}\text{C}$ -Acetyl Coenzyme A. 25  $\mu\text{g}$  of protein extract were loaded per lane. The source in lanes E1-E11 were SC82 transformants; B13 is a BMS (Black Mexican Sweet corn nonembryogenic) *bar* transformant. EO is a nonselected, nontransformed control.

As can be seen at the position indicated by the arrow (the position expected for the mobility of  $^{14}\text{C}$ -N-AcPPT), all lanes except the nontransformed control have activities with the appropriate mobility. Variation in activity among the transformants was approximately 10 fold, as demonstrated by the relative intensity of the bands. The results of this assay provide confirmation of the expression of the *bar* gene which codes for PAT. For analysis of PAT activity in plant tissue, 100-200 mg of leaf tissue was extracted in sintered glass homogenizers and assayed as described previously.

GUS activity was assessed histochemically as described using 5-bromo-4-chloro-3-indolyl glucuronide (Jefferson, 1987); tissue was scored for blue cells 18-24 h after addition of substrate. Fluorometric analysis was performed as described by Jefferson (1987) using 4-methyl umbelliferyl glucuronide.

DNA gel blot analysis was performed as follows. Genomic DNA was isolated using a procedure modified from Shure, et al., 1983. Approximately 1 gm callus tissue was ground to a fine powder in liquid N<sub>2</sub> using a mortar and pestle. Powdered tissue was mixed thoroughly with 4 ml extraction buffer (7.0 M urea, 0.35 M NaCl, 0.05 M Tris-HCl pH 8.0, 0.01 M EDTA, 1% sarcosine). Tissue/buffer homogenate was extracted with 4 ml phenol/ chloroform. The aqueous phase was separated by centrifugation, passed through Miracloth, and precipitated twice using 1/10 volume of 4.4 M ammonium acetate, pH 5.2 and an equal volume of isopropanol. The precipitate was washed with 70% ethanol and resuspended in 200-500  $\mu\text{l}$  TE (0.01 M Tris-HCl, 0.001 M EDTA, pH 8.0). Plant tissue may also be employed for the isolation of DNA using the foregoing procedure.

Genomic DNA was digested with a 3-fold excess of restriction enzymes, electrophoresed through 0.8% agarose (FMC), and transferred (Southern, 1975) to Nytran (Schleicher and Schuell) using 10X SCP (20X SCP: 2 M NaCl, 0.6 M disodium phosphate, 0.02 M disodium EDTA). Filters were prehybridized at 65°C in 6X SCP, 10% dextran sulfate, 2% sarcosine, and 500  $\mu\text{g}/\text{ml}$  heparin (Chomet, et al., 1987) for 15 min. Filters were hybridized overnight at 65°C in 6X SCP containing 100  $\mu\text{g}/\text{ml}$  denatured salmon sperm DNA and  $^{32}\text{P}$ -labeled probe. The 0.6 kb SmaI fragment from pDPG165 and the 1.8 kb BamHI/EcoRI fragment from pCEV5 were used in random priming reactions (Feinberg and Vogelstein, 1983; Boehringer-Mannheim) to generate labeled probes for detecting sequences encoding PAT or GUS, respectively. Filters were washed in 2X SCP, 1% SDS at 65°C for 30 min. and visualized by autoradiography using Kodak XAR5 film. Prior to rehybridization with a second probe, the filters were boiled for 10 min. in distilled H<sub>2</sub>O to remove the first probe and then prehybridized as described above.

### Example 9: Herbicide Application

The herbicide formulation used, Basta TX<sup>R</sup>, contains 200 g/l glufosinate, the ammonium salt of phosphinothricin. Young leaves were painted with a 2% Basta solution (v/v) containing 0.1% (v/v) Tween-20. The prescribed application rate for this formulation is 0.5-1%.

In Figure 10A, Basta<sup>R</sup> solution was applied to a large area (about 4 x 8 cm) in the center of leaves of a nontransformed A188 X B73 plant (left) and a transgenic R<sub>0</sub> E3/E4/E6 plant (right). In Figure 10B, Basta was also applied to leaves of four R<sub>1</sub> plants; two plants without *bar* and two plants containing *bar*. The herbicide was applied to R<sub>1</sub> plants in 1 cm circles to four locations on each leaf, two on each side of the midrib. Photographs were taken six days after application.

### K. Fertility of Transgenic Plants

To recover progeny the regenerated, genetically transformed maize plants (designated R<sub>0</sub>), were backcrossed with pollen collected from nontransformed plants derived from seeds, and progeny (designated R<sub>1</sub>) that contained and expressed *bar* were recovered.

An important aspect of this invention is the production for the first time of fertile, genetically transformed maize plants (R<sub>0</sub>) and progeny (R<sub>1</sub>). These were regenerated from embryogenic cells that were transformed. R<sub>1</sub> plants are those resulting from backcrossing of R<sub>0</sub> plants.

Pollination of transgenic R<sub>0</sub> ears with non-transformed B73 pollen resulted in kernel development. In addition, kernels developed from pistillate flowers on male inflorescences that were pollinated with non-transformed B73 pollen. Kernels on transformed R<sub>0</sub> plants from SC82 developed normally for approximately 10-14 days post-pollination but after this period the kernels ceased development and often collapsed. Most plants exhibited premature senescence at this time. A total of 153 kernels developed sporadically on numerous plants (see Table 5): 8 of 37 E2/E5 plants, 2 of 22 E10 plants, and 3 of 6 E11 plants. Viable progeny were recovered by embryo rescue from 11 E2/E5 plants and one E10 plant.

Table 5. Regenerated Plants (R<sub>0</sub>) and progeny (R<sub>1</sub>)

Exp #	Culture Bombarded	# of Independent bar Transformants Recovered	# of Regenerable Transformed Callus Lines	# of R <sub>0</sub> Plants	# Reaching Maturity	# of R <sub>0</sub> Producing Kernels	# of Kernels Recovered	# of R <sub>1</sub> Plants
1,2	SC82	7	4	76	73	23	153	40
4,5	SC716	20	10	219	(35)	(9)	(51)	(31)
3	SC94	8	2*	11*	(0)	(0)	(0)	(0)
6	SC82	19	4*	23*	(0)	(0)	(0)	(0)

\* Regeneration in progress.

() Experiment still in progress, data still being collected.

SC716  $R_0$  plants were also backcrossed with seed-derived B73 plants. To date, from the 35 mature SC716  $R_0$  plants nine plants (representing four independent callus lines) yielded 51 kernels, 31 of which produced vigorous  $R_1$  seedlings (Table 5). Most kernels that developed on SC716 plants did not require embryo rescue. Kernels often developed for 30-40 days on the plant and some were germinated in soil. The remaining seed was germinated on MS-based medium to monitor germination and transferred to soil after a few days. In addition to the improved kernel development observed on SC716  $R_0$  plants relative to SC82  $R_0$  plants, pollen dehiscence from anthers of several SC716 plants and some of this pollen germinated *in vitro* (Pfahler 1967). Transmission of the foreign gene has occurred both through SC716  $R_1$  ears and using SC716  $R_1$ -derived pollen on non-transformed ears.

Pollen obtained from transformed  $R_1$  plants has now been successfully employed to pollinate B73 ears and a large number of seeds have been recovered (see Figure 11C). Moreover, a transformed ear from an  $R_1$  plant crossed with pollen from a non-transformed inbred plant is shown in Figure 11D. The fertility characteristics of the  $R_1$  generation has been confirmed both from a standpoint of the pollen's ability to fertilize non-transformed ears, and the ability of  $R_1$  ears to be fertilized by pollen from non-transformed plants.

#### Example 10: Analysis of Progeny ( $R_1$ ) of Transformed $R_0$ Plants for PAT and *bar*

A total of 40 progeny of E2/E5  $R_0$  plants were analyzed for PAT activity, ten of which are shown in Figure 7A. Of 36 progeny which were assayed, 18 had PAT activity. Genomic DNA from the same ten progeny analyzed for PAT activity was analyzed by DNA gel blot hybridization for the presence of *bar* as shown in Figure 7B. The six progeny tested that expressed PAT contained a single copy of *bar* identical in mobility to that detected in callus and  $R_0$  plants; the four PAT-negative progeny tested did not contain *bar*-hybridizing sequences. In one series of assays, the presence of the *bar* gene product in 18 of 36 progeny indicates a 1:1 segregation of the single copy of *bar* found in E2/E5  $R_0$  plants and is consistent with inheritance of PAT expression as a single dominant trait. A dominant pattern of inheritance would indicate the presence in the plant of at least one copy of the gene coding for PAT. The single progeny recovered from an E10  $R_0$  plant tested positive for PAT activity.

It was determined that the methods disclosed in this invention resulted in transformed  $R_0$  and  $R_1$  plants that produced functionally active PAT. This was determined by applying Basta (PPT) to the leaves of plants and determining whether necrosis (tissue destruction) resulted from this application. If functionally active PAT is produced by the plants, the leaf tissue is protected from necrosis. No necrosis was observed on  $R_0$  plants expressing high levels of PAT (E2/E5) or on plants expressing low levels (E3/E4/E6) (Fig. 10A).

Herbicide was also applied to leaves of  $R_1$  progeny segregating for *bar*. In these studies, no necrosis was observed on  $R_1$  plants containing and expressing *bar*, however, necrosis was observed on those  $R_1$  plants lacking the *bar* gene. This is shown in Fig 10B.

Segregation of *bar* did not correlate with the variability in phenotypic characteristics of  $R_1$  plants such as plant height and tassel morphology. In Figure 9B, the plant on the right contains *bar*, the plant on the left does not. In addition, most of the  $R_1$  plants were more vigorous than the  $R_0$  plants.

Of the 23  $R_1$  seedlings recovered to date from the SC716 transformants, ten of 16 had PAT activity. PAT activity was detected in four of ten progeny from  $R_0$  plants representing callus line R18 and six of six progeny from  $R_0$  plants representing callus line R9.

#### L. Embryo Rescue

In cases where embryo rescue was required, developing embryos were excised from surface disinfected kernels 10-20 days post-pollination and cultured on medium containing MS salts, 2% sucrose and 5.5 g/l Seakem agarose. Large embryos (>3 mm) were germinated directly on the medium described above. Smaller embryos were cultured for approximately 1 week on the above medium containing  $10^{-5}$ M abscisic acid and transferred to hormone-free medium for germination. Several embryos became bacterially contaminated; these embryos were transferred to medium containing 300  $\mu$ g/ml cefoxitin. Developing plants were subsequently handled as described for regeneration of  $R_0$  plants.

#### Example 11: Embryo Rescue

Viable progeny, recovered from seven SC82 E2/E5 plants and one SC82 E10 plant, were sustained by embryo rescue. This method consisted of excising embryos from kernels that developed on  $R_0$  plants. Embryos ranged in size from about 0.5 to 4 mm in length. Small e-bryos were cultured on maturation medium containing abscisic acid while larger embryos were cultured directly on germination medium. Two of the approximately forty viable progeny thus far recovered from SC82  $R_0$  plants are shown in Figure 11B.

## M. Phenotype of Transgenic Plants

Most of the  $R_0$  plants regenerated from SC82 transformants exhibited an A188 X B73 hybrid phenotype. Plants were similar in height to seed derived A188 plants (3-5 feet) but had B73 traits such as anthocyanin accumulation in stalks and prop roots, and the presence of upright leaves. Many plants, regardless of the callus line from which they were regenerated, exhibited phenotypic abnormalities including leaf splitting, forked leaves, multiple ears per node, and coarse silk. Although many of the phenotypic characteristics were common to all  $R_0$  plants, some characteristics were unique to plants regenerated from specific callus lines. Such characteristics were exhibited regardless of regeneration route and the time spent in culture during regeneration.

Nontransformed control plants were not regenerated from this culture and, therefore, cannot be compared phenotypically. Pistillate flowers developed on tassels of one E11 (1/6), several E10 (3/22) and almost one-third of the E2/E5 (12/37) plants with a range of three to approximately twenty ovules per tassel. Primary and secondary ears developed frequently on most E2/E5, E10, and E11 plants; a mature E2/E5 plant is shown in Figure 11A. Anthers rarely extruded from the tassels of plants regenerated from SC82 transformants and the limited number of anthers which were extruded did not dehisce pollen. Some phenotypic characteristics observed were unique to plants regenerated from a specific callus line such as the lack of ears on E3/E4/E6 plants and a "grassy" phenotype (up to 21 lone narrow leaves) exhibited by all E11 plants.

All SC82 plants senesced prematurely; leaf necrosis began approximately two weeks after anthesis. The  $R_0$  plants regenerated from SC82 transformed cell lines have tended to senesce prematurely; typically before the developing kernels were mature. This has necessitated the use of embryo rescue to recover progeny ( $R_1$  generation). Segregation of *bar* in the  $R_1$  generation does not correlate with the variability in phenotypic characteristics of  $R_1$  plants such as plant height and tassel morphology. In Figure 11B, the plant on the right contains *bar*, the plant on the left does not. In addition, most of the  $R_1$  plants are more vigorous than the  $R_0$  plants. Transformed progeny ( $R_1$ ) have now also begun to yield kernels and  $R_2$  plantlets have been recovered.

Of 219 plants regenerated from 10 independent SC716 transformants, approximately 35 have reached maturity (Table 5). The SC716 plants did not exhibit the phenotypic differences which characterized the individual callus lines of SC82. These plants were more uniform and abnormalities less frequent. The phenotype of these plants closely resembled that of control plants regenerated from a SC716 cryopreserved culture which was not bombarded. Plant height ranged from three to six feet with the majority of the plants between five and six feet. Most mature plants produced large, multi-branched tassels and primary and secondary ears. Pistillate flowers also developed on tassels of several SC716 plants. Although anther extrusion occurred at approximately the same low frequency as in the SC82 plants, a small amount of pollen dehisced from some extruded anthers. For most of the SC716 plants that reached maturity, senescence did not commence until at least 30 days after anthesis. The improved characteristics of SC716 plants over SC82 plants indicate that differences between the suspension cultures may be responsible.

While the invention is susceptible to various modifications and alternative forms, specific embodiments thereof have been shown by way of example in the drawings and herein be described in detail. It should be understood, however, that it is not intended to limit the invention to the particular forms disclosed, but on the contrary, the intention is to cover all modifications, equivalents, and alternatives falling within the spirit and scope of the invention as defined by the appended claims.

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## Claims

1. A method for the production of fertile, transgenic maize plants, said method comprising the steps of:
  - (a) preparing a DNA composition, a component of which one desires to have expressed in, or introduced into the genome of, a maize plant;
  - (b) contacting recipient maize cells with said DNA composition under conditions allowing the uptake of DNA by the recipient cells, said contact being effected by using micro-projectile bombardment;
  - (c) regenerating maize plants from the recipient cells, which have received the DNA component; and
  - (d) identifying fertile, transgenic maize plants containing the desired DNA component.
2. The method of claim 1, wherein said recipient cells comprise callus cells, gametic cells, meristematic cells, immature embryo cells or embryonic maize cells.
3. The method of claim 1 or 2, wherein said recipient cells comprise cells obtained from suspension culture, particularly wherein said suspension culture is prepared from an embryogenic callus.
4. The method of any of claims 1 to 3, wherein the DNA composition comprises a plasmid, preferably a plasmid comprising a transposable element, particularly a transposable element comprising an Ac, Ds or Mu element.
5. The method of any of claims 1 to 4, wherein the DNA composition comprises an exogenous gene, and optionally, a promoter and 3' region operatively linked to said exogenous gene, preferably a CaMV 35S, CaMV 19S, nos, Adh, sucrose synthase, R-allele or root cell promoter.
6. The method of claim 5, wherein the exogenous gene comprises a selectable or screenable marker gene, particularly a marker gene comprising a neo gene, a GUS gene, a bar gene, a mutant EPSP synthase gene, a nitrilase gene, an acetolactate synthase gene, a gene from the R complex, and/or a maize gene and/or a gene encoding a desired trait, particularly a herbicide resistance gene, an insect resistance gene, an antifreeze protein gene, or an antifungal gene.
7. The method of claim 6, wherein the exogenous gene comprises a neo gene.

8. The method of claim 6, wherein the exogenous gene comprises a GUS gene.
9. The method of claim 6, wherein the exogenous gene comprises a bar gene.
- 5 10. The method of claim 6, wherein the exogenous gene comprises a mutant EPSP synthase gene.
11. The method of claim 6, wherein the exogenous gene comprises a nitrilase gene.
12. The method of claim 6, wherein the exogenous gene comprises a gene from the R gene complex.
- 10 13. The method of claim 6, wherein the exogenous gene comprises an acetolactate synthase gene.
14. The method of claim 6, wherein the exogenous gene comprises a herbicide resistance gene.
- 15 15. The method of claim 14, wherein the herbicide resistance gene comprises a phosphinothricin resistance gene.
16. The method of claim 14, wherein the herbicide resistance gene comprises a glyphosate resistance gene.
17. The method of claim 6, wherein the exogenous gene comprises an insect resistance gene.
- 20 18. The method of claim 17, wherein the insect resistance gene comprises a *Bacillus thuringiensis* toxin gene.
19. The method of claim 6, wherein the exogenous gene comprises an antifungal gene.
- 25 20. The method of claim 19, wherein the antifungal gene comprises a hevein or chitinase gene.
21. The method of claim 6, wherein the exogenous gene comprises a maize gene.
- 30 22. The method of any of the preceding claims, wherein the recipient cells are cotransformed with more than one exogenous gene, and, preferably, wherein at least two exogenous genes are positioned on the same DNA segment, and recipient cells are contacted with said segment.
23. The method of any of the preceding claims, wherein the recipient maize cells receiving the DNA composition are selected for following introduction of the DNA composition therein.
- 35 24. The method of any of claim 23, wherein the recipient cells, which have received a DNA component, are selected for prior to regeneration, particularly by incubation in contact with a selective medium, particularly on a selective medium which comprises bialaphos or PPT.
- 40 25. The method of any of the preceding claims, further comprising the step of preparing a maize cell composition, which includes maize recipient cells, prior to contacting said recipient cells with said DNA composition, preferably wherein said maize cell composition has been subjected to cryopreservation prior to contacting it with the DNA composition.
- 45 26. The method of any of the preceding claims, wherein the recipient maize cells are selected for prior to the introduction of the DNA composition therein.
27. The method of claim 25 or 26, wherein the maize cell composition is prepared by:
  - 50 (a) preparing an embryogenic callus; and
  - (b) selecting cells from said callus, which cells comprise recipient cells and, optionally, culturing the selected callus cells in suspension culture prior to contacting them with the DNA composition.
- 55 28. The method of any of the preceding claims, wherein the uptake of the DNA composition by the recipient cells is achieved by microprojectile bombardment of the cells, by passing particles on which the DNA composition has been coated through a screen and into the cells, preferably wherein the particles comprise tungsten, gold or platinum.

29. The method of any of the preceding claims, wherein the embryonic cells are grown in a suspension culture comprising media with one or more hormones.

30. The method of any of the preceding claims, wherein the regeneration of maize plants from the recipient cells comprises the steps of:

(a) culturing maize recipient cells, which have received DNA in a medium comprising an embryogenic promoting hormone, preferably a medium comprising dicamba or 2,4-D, until callus organization is observed;

(b) transferring said cells to a medium, which includes a tissue organization promoting medium, in particular a medium comprising BAP, myoinositol and 2,4-D, and/or ABA, BAP, NAA, IAA, 2-IP or myoinositol;

(c) subculturing said cells onto media without said hormones, to allow for shoot elongation or root development;

(d) transferring said cells onto a minimal medium, preferably a medium comprising Clark's medium, to provide for hardening of the plant, and, optionally,

(e) applying to said cells a hormone, in particular IBA, to stimulate rooting.

31. The method of claim 30, wherein the medium employed for step (c) includes myoinositol.

32. The method of any of the preceding claims, further comprising the preparation of progeny plants of one of the identified fertile, transgenic maize plant, wherein said progeny plants contain the desired DNA component.

33. The method of claim 32, further comprising breeding one of the progeny plants with a maize plant, to prepare a bred plant, wherein said bred plant contains the desired DNA component.

34. The method of claim 33, wherein one of said progeny plants is bred with a non-transgenic maize plant, wherein said bred plant contains the desired DNA component.

35. The method of any of the preceding claims, further comprising preparing seed from one or more of the fertile, transgenic maize plants or progeny plants, wherein said seed contains the desired DNA component.

## Patentansprüche

1. Verfahren zur Herstellung von fruchtbaren transgenen Maispflanzen, wobei das Verfahren folgende Stufen umfaßt:

(a) Herstellung einer DNA-Zusammensetzung, wobei von einer Komponente der Zusammensetzung gewünscht wird, daß sie in einer Maispflanze exprimiert oder in das Genom einer Maispflanze eingeführt wird;

(b) Kontaktieren von Empfängermaiszellen mit der DNA-Zusammensetzung unter Bedingungen, die die Aufnahme von DNA durch die Empfängerzellen erlauben, wobei der Kontakt unter Anwendung des Mikroprojektilbombardements bewirkt wird;

(c) Regeneration von Maispflanzen aus den Empfängerzellen, die die DNA-Komponente empfangen haben; und

(d) Identifizierung fruchtbarer transgener Maispflanzen, die die gewünschte DNA-Komponente enthalten.

2. Verfahren nach Anspruch 1, wobei die Empfängerzellen Calluszellen, Gametenzellen, Meristemzellen, unreife Embryozellen oder embryogene Maiszellen umfassen.

3. Verfahren nach Anspruch 1 oder 2, wobei die Empfängerzellen Zellen umfassen, die aus einer Suspensionskultur erhalten wurden, wobei die Suspensionskultur insbesondere von einem embryogenen Callus hergestellt wird.

4. Verfahren nach einem der Ansprüche 1 bis 3, wobei die DNA-Zusammensetzung ein Plasmid umfaßt, vorzugsweise ein Plasmid, das ein transponierbares Element und insbesondere ein transponierbares Element, das ein Ac-, Ds- oder Mu-Element, umfaßt, umfaßt.

5. Verfahren nach einem der Ansprüche 1 bis 4, wobei die DNA-Zusammensetzung ein exogenes Gen und wahlweise

einen Promotor und eine 3'-Region in funktioneller Verknüpfung mit dem exogenen Gen und vorzugsweise einen CaMV 35S-, CaMV 19S-, nos-, Adh-, Saccharosesynthase-, R-Allel- oder Wurzelzellpromotor umfaßt.

- 5 6. Verfahren nach Anspruch 5, wobei das exogene Gen ein selektierbares oder absuchbares Markergen und insbesondere ein Markergen, das ein neo-Gen, ein GUS-Gen, ein bar-Gen, ein mutiertes EPSP-Synthase-Gen, ein Nitrilase-Gen, ein Acetolactat-Synthase-Gen, ein Gen aus dem R-Komplex und/oder ein Maisgen und/oder ein Gen, das für ein gewünschtes Merkmal kodiert, insbesondere ein Herbizid-Resistenzgen, ein Insekten-Resistenzgen, ein Frostschutzprotein-Gen oder ein Fungizid-Gen, umfaßt, umfaßt.
- 10 7. Verfahren nach Anspruch 6, wobei das exogene Gen ein neo-Gen umfaßt.
8. Verfahren nach Anspruch 6, wobei das exogene Gen ein GUS-Gen umfaßt.
9. Verfahren nach Anspruch 6, wobei das exogene Gen ein bar-Gen umfaßt.
- 15 10. Verfahren nach Anspruch 6, wobei das exogene Gen ein mutiertes EPSP-Synthase-Gen umfaßt.
11. Verfahren nach Anspruch 6, wobei das exogene Gen ein Nitrilase-Gen umfaßt.
- 20 12. Verfahren nach Anspruch 6, wobei das exogene Gen ein Gen aus dem R-Genkomplex umfaßt.
13. Verfahren nach Anspruch 6, wobei das exogene Gen ein Acetolactat-Synthase-Gen umfaßt.
14. Verfahren nach Anspruch 6, wobei das exogene Gen ein Herbizid-Resistenzgen umfaßt.
- 25 15. Verfahren nach Anspruch 14, wobei das Herbizid-Resistenzgen ein Phosphinothricin-Resistenzgen umfaßt.
16. Verfahren nach Anspruch 14, wobei das Herbizid-Resistenzgen ein Glyphosat-Resistenzgen umfaßt.
- 30 17. Verfahren nach Anspruch 6, wobei das exogene Gen ein Insekten-Resistenzgen umfaßt.
18. Verfahren nach Anspruch 17, wobei das Insekten-Resistenzgen ein Bacillus thuringiensis-Toxin-Gen umfaßt.
19. Verfahren nach Anspruch 6, wobei das exogene Gen ein Fungizid-Gen umfaßt.
- 35 20. Verfahren nach Anspruch 19, wobei das Fungizid-Gen ein Heveinoder Chitinase-Gen umfaßt.
21. Verfahren nach Anspruch 6, wobei das exogene Gen ein Maisgen umfaßt.
- 40 22. Verfahren nach einem der vorstehenden Ansprüche, wobei die Empfängerzellen mit mehr als einem exogenen Gen cotransformiert werden, wobei vorzugsweise mindestens zwei exogene Gene auf dem gleichen DNA-Segment angeordnet sind, und Empfängerzellen mit dem Segment in Kontakt gebracht werden.
23. Verfahren nach einem der vorstehenden Ansprüche, wobei die Empfängermaiszellen, die die DNA-Zusammensetzung empfangen, nach der Einführung der DNA-Zusammensetzung selektiert werden.
- 45 24. Verfahren nach Anspruch 23, wobei die Empfängerzellen, die eine DNA-Komponente erhalten haben, vor der Regeneration selektiert werden, insbesondere durch Inkubation in Kontakt mit einem selektiven Medium, insbesondere auf einem selektiven Medium, das Bialaphos oder PPT umfaßt.
- 50 25. Verfahren nach einem der vorstehenden Ansprüche, das ferner die Stufe der Herstellung einer Maiszellzusammensetzung, die Maisempfängerzellen umfaßt, vor dem Kontaktieren der Empfängerzellen mit der DNA-Zusammensetzung umfaßt, wobei die Maiszellzusammensetzung vorzugsweise einer Tiefkühlkonservierung vor dem Kontaktieren mit der DNA-Zusammensetzung unterzogen worden ist.
- 55 26. Verfahren nach einem der vorstehenden Ansprüche, wobei die Empfängermaiszellen vor der Einführung der DNA-Zusammensetzung selektiert werden.

27. Verfahren nach Anspruch 25 oder 26, wobei die Maiszellzusammensetzung hergestellt wird durch:

- (a) Herstellung eines embryogenen Callus; und
- (b) Selektion von Zellen aus dem Callus, wobei die Zellen Empfängerzellen umfassen, und wahlweise Kultivieren der selektierten Calluszellen in Suspensionskultur vor dem Kontaktieren mit der DNA-Zusammensetzung.

28. Verfahren nach einem der vorstehenden Ansprüche, wobei die Aufnahme der DNA-Zusammensetzung durch die Empfängerzellen durch Mikroprojektilbombardement der Zellen erzielt wird, indem Partikel, auf die die DNA-Zusammensetzung aufgebracht worden ist, durch ein Sieb und in die Zellen geführt werden, wobei die Partikel vorzugsweise Wolfram, Gold oder Platin umfassen.

29. Verfahren nach einem der vorstehenden Ansprüche, wobei die embryogenen Zellen in einer Suspensionskultur gezüchtet werden, die Medien mit einem oder mehreren Hormonen umfaßt.

30. Verfahren nach einem der vorstehenden Ansprüche, wobei die Regeneration der Maispflanzen aus den Empfängerzellen die folgenden Stufen umfaßt:

- (a) Kultivieren von Maisempfängerzellen, die DNA empfangen haben, in einem Medium, das ein embryogenes Förderhormon umfaßt, vorzugsweise einem Medium, das Dicamba oder 2,4-D umfaßt, bis eine Callusorganisation beobachtet wird;
- (b) Übertragung der Zellen aus einem Medium, das ein die Gewebeorganisation förderndes Medium umfaßt, insbesondere ein Medium, das BAP, Myoinosit und 2,4-D und/oder ABA, BAP, NAA, IAA, 2-IP oder Myoinosit umfaßt;
- (c) Subkultivieren der Zellen auf Medien ohne diese Hormone, um eine Sproßverlängerung oder eine Wurzelentwicklung zu ermöglichen;
- (d) Übertragung der Zellen auf ein minimales Medium und vorzugsweise ein Medium, das Clark-Medium umfaßt, um für eine Abhärtung der Pflanze zu sorgen; und wahlweise
- (e) Auftragen eines Hormons, insbesondere IBA, auf die Zellen, um die Wurzelbildung zu stimulieren.

31. Verfahren nach Anspruch 30, wobei das für Stufe (c) eingesetzte Medium Myoinosit umfaßt.

32. Verfahren nach einem der vorstehenden Ansprüche, das ferner die Herstellung von Nachkommenpflanzen einer der identifizierten fruchtbaren transgenen Maispflanzen umfaßt, wobei die Nachkommenpflanzen die gewünschte DNA-Komponente enthalten.

33. Verfahren nach Anspruch 32, das ferner die Züchtung einer der Nachkommenpflanzen mit einer Maispflanze zur Herstellung einer gezüchteten Pflanze umfaßt, wobei die gezüchtete Pflanze die gewünschte DNA-Komponente enthält.

34. Verfahren nach Anspruch 33, wobei eine der Nachkommenpflanzen mit einer nicht-transgenen Maispflanze gezüchtet wird, wobei die gezüchtete Pflanze die gewünschte DNA-Komponente enthält.

35. Verfahren nach einem der vorstehenden Ansprüche, das ferner die Herstellung von Samen aus einer oder mehreren fruchtbaren transgenen Maispflanzen oder Nachkommenpflanzen umfaßt, wobei der Samen die gewünschte DNA-Komponente enthält.

## Revendications

1. Procédé de production de plants de maïs transgéniques, fertiles, ledit procédé comportant les étapes consistant à :

- (a) préparer une composition d'ADN, dont on veut faire exprimer un composant dans un plant de maïs, ou dont on veut introduire un composant dans le génome de celui-ci ;
- (b) mettre en contact des cellules receveuses de maïs avec ladite composition d'ADN sous des conditions permettant l'absorption de l'ADN par les cellules receveuses, ladite mise en contact étant effectuée en utilisant un bombardement de micro-projectiles ;
- (c) régénérer des plants de maïs à partir des cellules receveuses, qui ont reçu le composant d'ADN ; et

(d) identifier les plants de maïs transgéniques, fertiles contenant le composant d'ADN voulu.

2. Procédé selon la revendication 1, dans lequel lesdites cellules receveuses comportent des cellules de cal, des cellules gamétiques, des cellules méristématiques, des cellules d'embryons immatures ou des cellules embryonnaires de maïs.
3. Procédé selon la revendication 1 ou 2, dans lequel lesdites cellules receveuses comportent des cellules obtenues à partir d'une culture en suspension, en particulier dans lequel ladite culture en suspension est préparée à partir d'un cal embryogène.
4. Procédé selon l'une quelconque des revendications 1 à 3, dans lequel la composition d'ADN comporte un plasmide, de préférence un plasmide comportant un élément transposable, en particulier un élément transposable comportant un élément Ac, Ds ou Mu.
5. Procédé selon l'une quelconque des revendications 1 à 4, dans lequel la composition d'ADN comporte un gène étranger, et en option, un promoteur et une région 3' liés de manière opérationnelle audit gène étranger, de préférence un promoteur du 35S de CaMV, du 19S de CaMV, de nos, de l'Adh, de la saccharose synthétase, de l'allele-R ou de cellule de racine.
6. Procédé selon la revendication 5, dans lequel le gène étranger comporte un gène marqueur pouvant être sélectionné ou criblé, en particulier un gène marqueur comportant un gène néo, un gène GUS, un gène bar, un gène mutant de l'EPSP synthétase, un gène de nitrilase, un gène de l'acétolactate synthétase, un gène provenant du complexe R, et/ou un gène de maïs et/ou un gène codant pour un trait voulu, en particulier un gène de résistance aux herbicides, un gène de résistance aux insectes, un gène de protéine de résistance au gel, ou un gène d'antifongique.
7. Procédé selon la revendication 6, dans lequel le gène étranger comporte un gène néo.
8. Procédé selon la revendication 6, dans lequel le gène étranger comporte un gène GUS.
9. Procédé selon la revendication 6, dans lequel le gène étranger comporte un gène bar.
10. Procédé selon la revendication 6, dans lequel le gène étranger comporte un gène mutant de l'EPSP synthétase.
11. Procédé selon la revendication 6, dans lequel le gène étranger comporte un gène de nitrilase.
12. Procédé selon la revendication 6, dans lequel le gène étranger comporte un gène provenant du complexe génique R.
13. Procédé selon la revendication 6, dans lequel le gène étranger comporte un gène de l'acétolactate synthétase.
14. Procédé selon la revendication 6, dans lequel le gène étranger comporte un gène de résistance aux herbicides.
15. Procédé selon la revendication 14, dans lequel le gène de résistance aux herbicides comporte un gène de résistance à la phosphinotricine.
16. Procédé selon la revendication 14, dans lequel le gène de résistance aux herbicides comporte un gène de résistance au glyphosate.
17. Procédé selon la revendication 6, dans lequel le gène étranger comporte un gène de résistance aux insectes.
18. Procédé selon la revendication 17, dans lequel le gène de résistance aux insectes comporte un gène d'une toxine de *Bacillus thuringiensis*.
19. Procédé selon la revendication 6, dans lequel le gène étranger comporte un gène d'antifongique.
20. Procédé selon la revendication 18, dans lequel le gène d'antifongique comporte un gène d'hévéine ou de chitinase.



21. Procédé selon la revendication 6, dans lequel le gène étranger comporte un gène de maïs.
22. Procédé selon l'une quelconque des revendications précédentes, dans lequel les cellules receveuses sont co-transformées à l'aide de plus d'un gène étranger, et, de préférence, dans lequel au moins deux gènes étrangers sont disposés sur le même segment d'ADN, et les cellules receveuses sont mises en contact avec ledit segment.
23. Procédé selon l'une quelconque des revendications précédentes, dans lequel les cellules receveuses de maïs recevant la composition d'ADN sont sélectionnées pour suivre l'introduction de la composition d'ADN à l'intérieur de celles-ci.
24. Procédé selon la revendication 23, dans lequel les cellules receveuses, qui ont reçu un composant d'ADN, sont sélectionnées avant régénération, en particulier par incubation en présence d'un milieu sélectif, en particulier sur un milieu sélectif qui comporte du bialaphos ou du PPT.
25. Procédé selon l'une quelconque des revendications précédentes, comportant de plus l'étape de préparation d'une composition de cellules de maïs, qui comporte des cellules receveuses de maïs, avant de mettre en contact lesdites cellules receveuses avec ladite composition d'ADN, de préférence dans lequel ladite composition de cellules de maïs a été soumise à une cryo-conservation avant d'être mise en contact avec la composition d'ADN.
26. Procédé selon l'une quelconque des revendications précédentes, dans lequel les cellules receveuses de maïs sont sélectionnées avant l'introduction de la composition d'ADN à l'intérieur de celles-ci.
27. Procédé selon la revendication 25 ou 26, dans lequel la composition de cellules de maïs est préparée par :
  - (a) préparation d'un cal embryogène ; et
  - (b) sélection des cellules provenant dudit cal, lesquelles cellules comportent des cellules receveuses et, en option, par culture des cellules de cal sélectionnés en culture en suspension avant de les mettre en contact avec la composition d'ADN.
28. Procédé selon l'une quelconque des revendications précédentes, dans lequel l'absorption de la composition d'ADN par les cellules receveuses est obtenue par bombardement des cellules à l'aide de micro-projectiles, en faisant passer des particules revêtues de la composition d'ADN à travers une plaque de rétention et en les faisant pénétrer dans les cellules, procédé dans lequel les particules comportent de préférence du tungstène, de l'or ou du platine.
29. Procédé selon l'une quelconque des revendications précédentes, dans lequel les cellules embryonnaires sont mises à pousser dans une culture en suspension comportant des milieux ayant une ou plusieurs hormones.
30. Procédé selon l'une quelconque des revendications précédentes, dans lequel la régénération des plants de maïs à partir des cellules receveuses comporte les étapes consistant à :
  - (a) cultiver les cellules receveuses de maïs, qui ont reçu l'ADN sur un milieu comportant une hormone favorisant l'embryogenèse, de préférence un milieu comportant du dicamba ou du 2,4-D, jusqu'à ce qu'une organisation en cal soit observée ;
  - (b) transférer lesdites cellules sur un milieu, qui comporte un milieu favorisant l'organisation en tissu, en particulier un milieu comportant du BAP, du myoinositol et du 2,4-D, et/ou de l'ABA, du BAP, du NAA, du IAA, du 2-IP ou du myoinositol ;
  - (c) sous-cultiver lesdites cellules sur des milieux exempts desdites hormones, pour permettre une elongation de la pousse ou un développement de racines ;
  - (d) transférer lesdites cellules sur un milieu minimal, de préférence un milieu comportant un milieu de Clark, pour fournir un affermissement du plant, et, en option,
  - (e) appliquer auxdites cellules une hormone, en particulier l'IBA, pour stimuler l'enracinement.
31. Procédé selon la revendication 30, dans lequel le milieu utilisé pour l'étape (c) comporte du myoinositol.
32. Procédé selon l'une quelconque des revendications précédentes, comportant de plus la préparation de plants de descendance de l'un des plants de maïs transgéniques identifiés, fertiles, dans lequel les plants de descendance contiennent le composant d'ADN voulu.

33. Procédé selon la revendication 32, comportant de plus le croisement d'un des plants de descendance avec un plant de maïs, pour préparer un plant issu de reproduction croisée, dans lequel ledit plant issu de reproduction croisée contient le composant d'ADN voulu.

5 34. Procédé selon la revendication 33, dans lequel un desdits plants de descendance est croisé avec un plant de maïs non-transgénique, dans lequel ledit plant issu de reproduction croisée contient le composant d'ADN voulu.

10 35. Procédé selon l'une quelconque des revendications précédentes, comportant en outre la préparation d'une semence à partir d'un ou de plusieurs plants de maïs transgéniques, fertiles ou plants de descendance, dans lequel ladite semence contient le composant d'ADN voulu.

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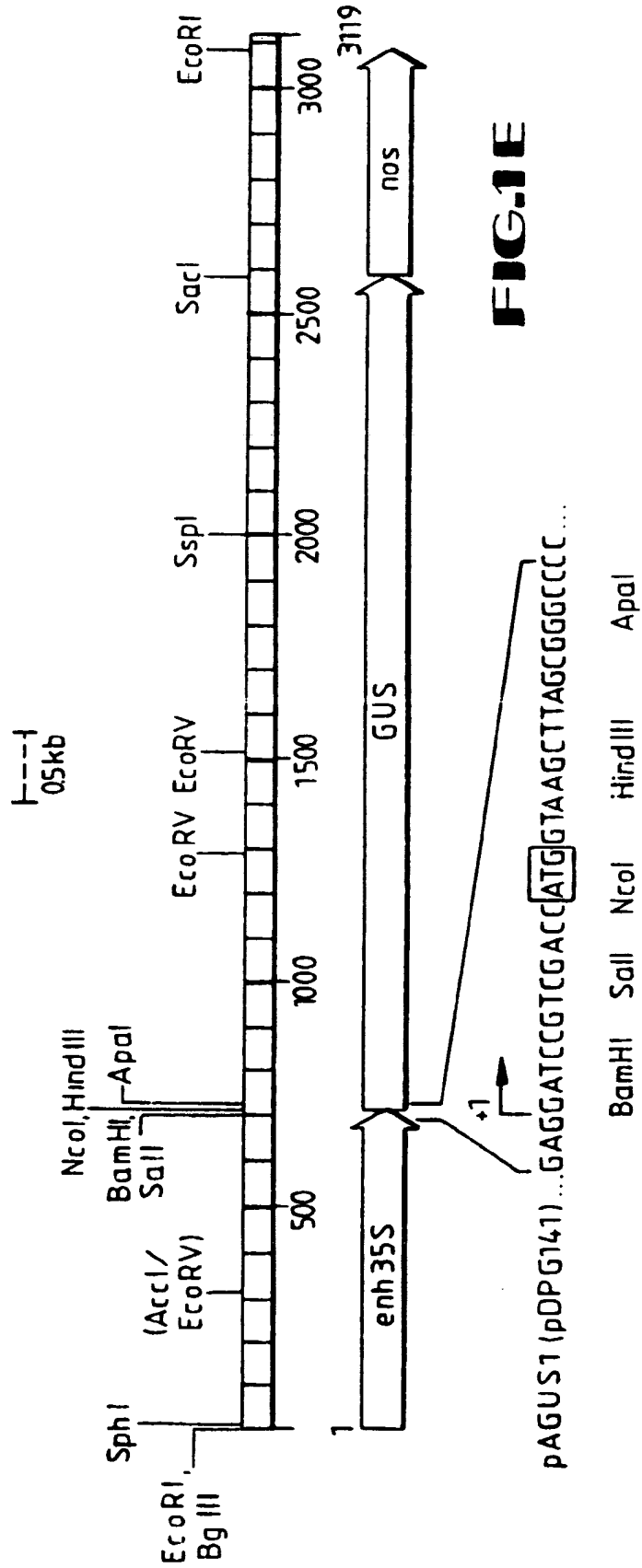
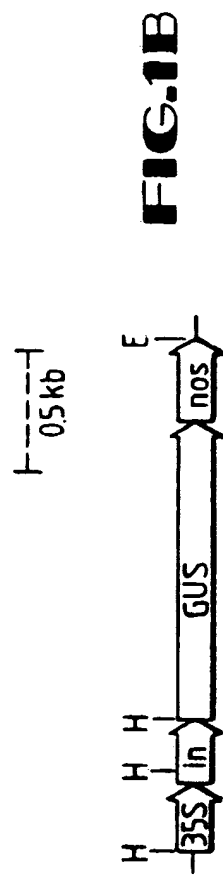
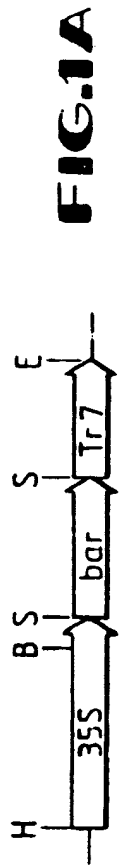
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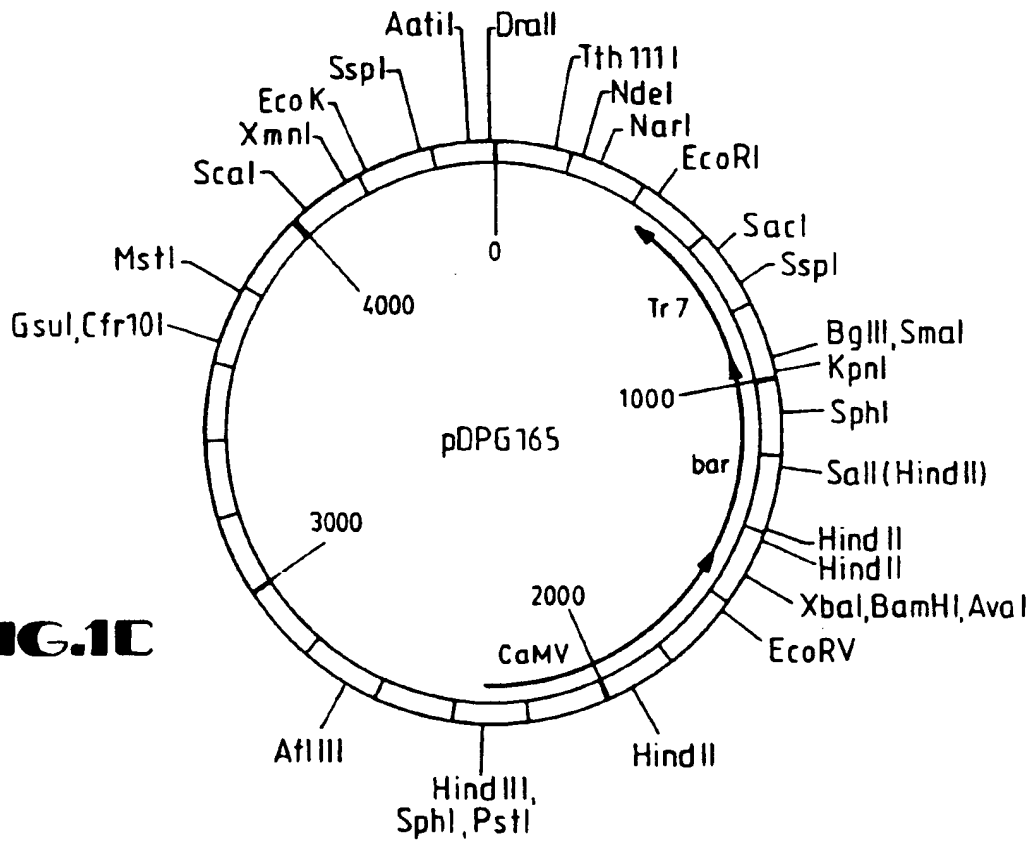
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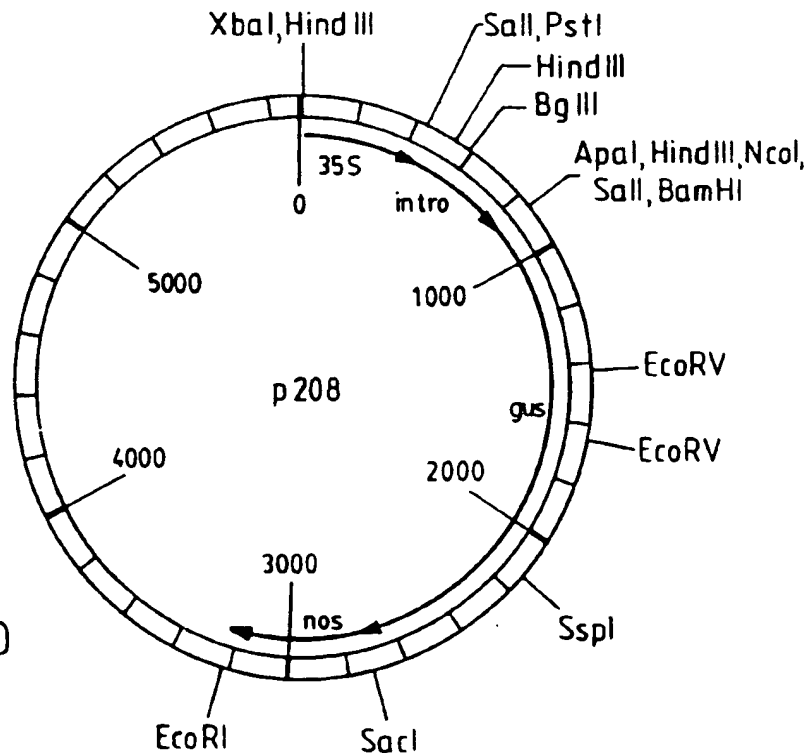
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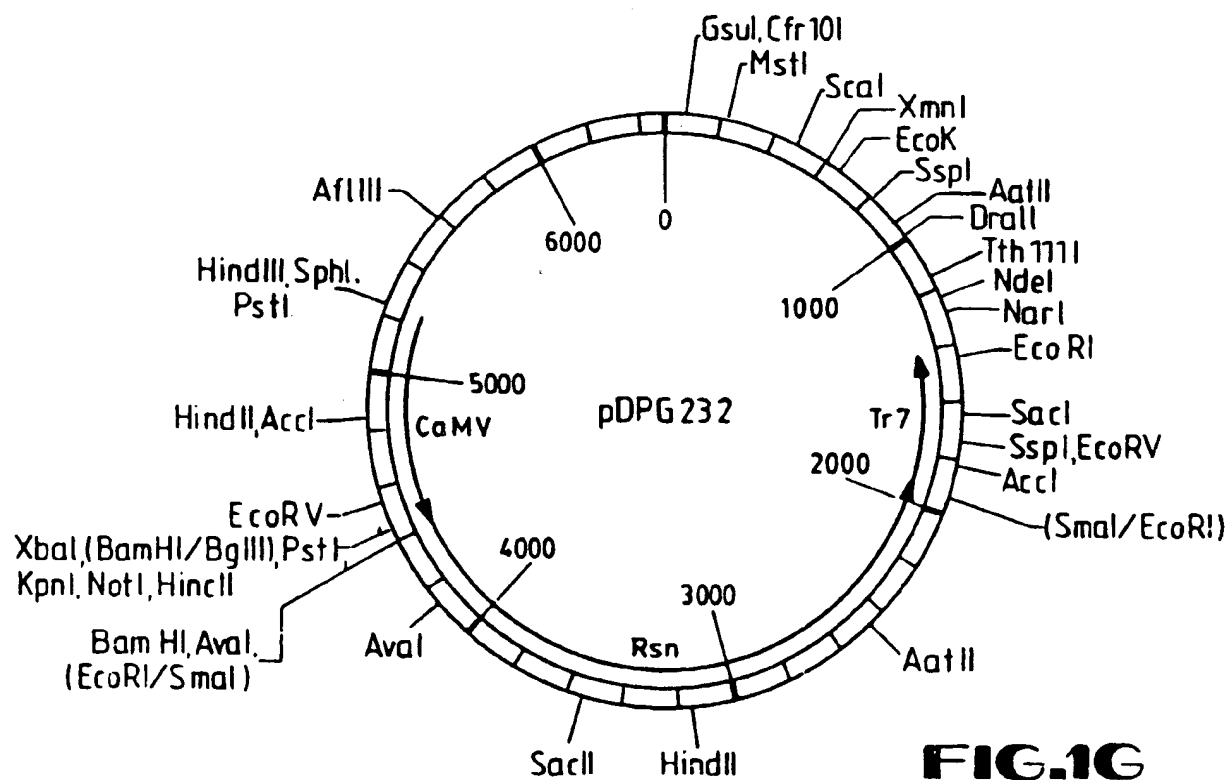
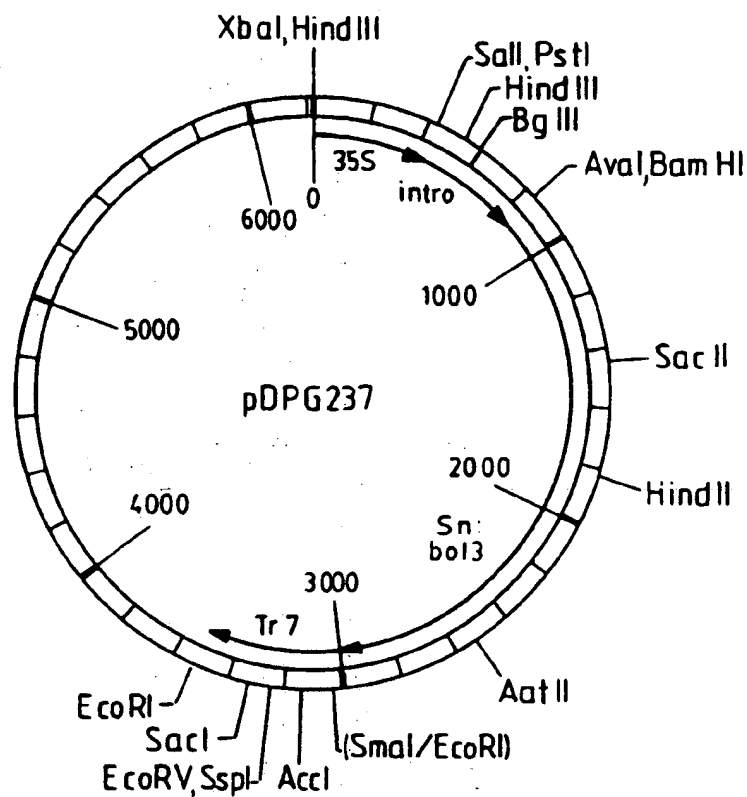
**FIG.1C**



**FIG.1D**

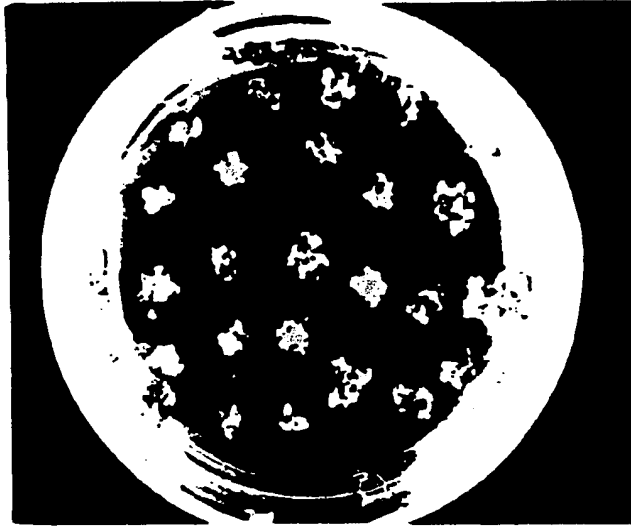


**FIG.1F**



**FIG.1G**

**FIG.2A**



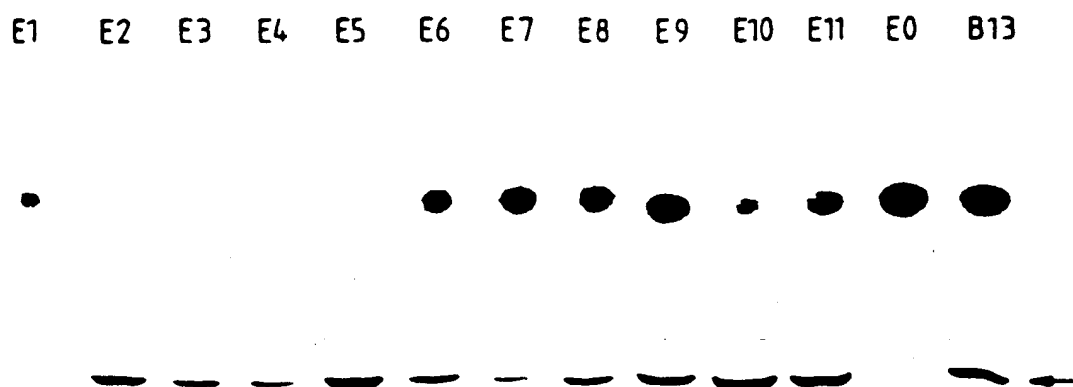
**FIG.2B**



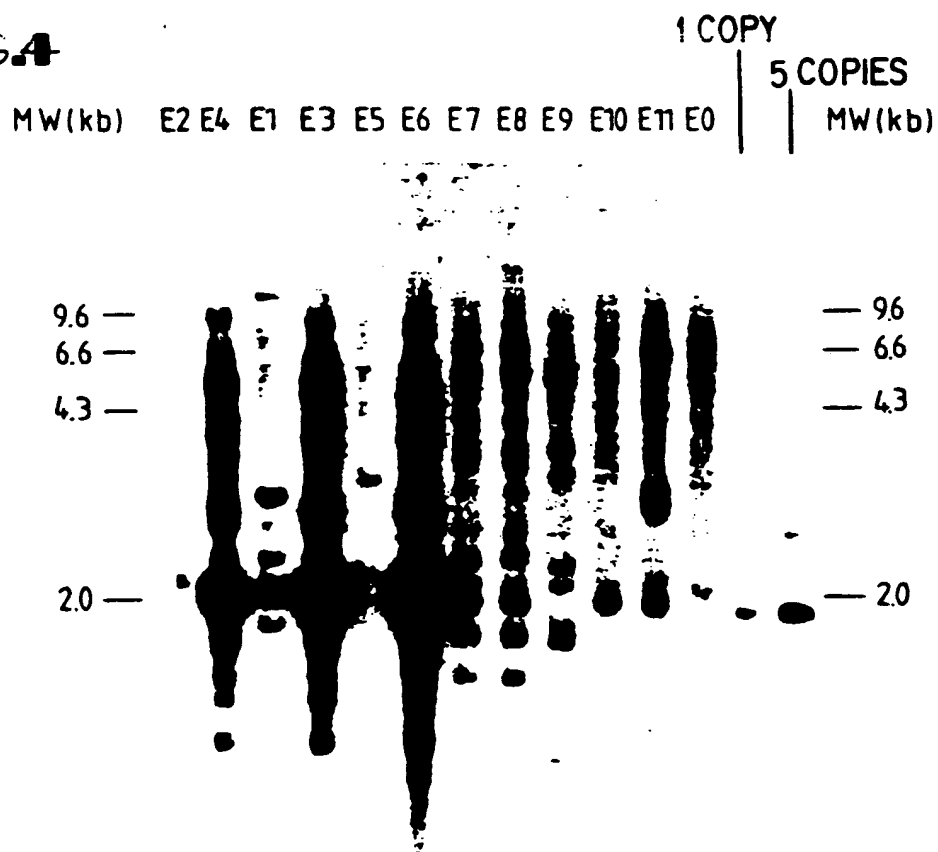
**FIG.8**



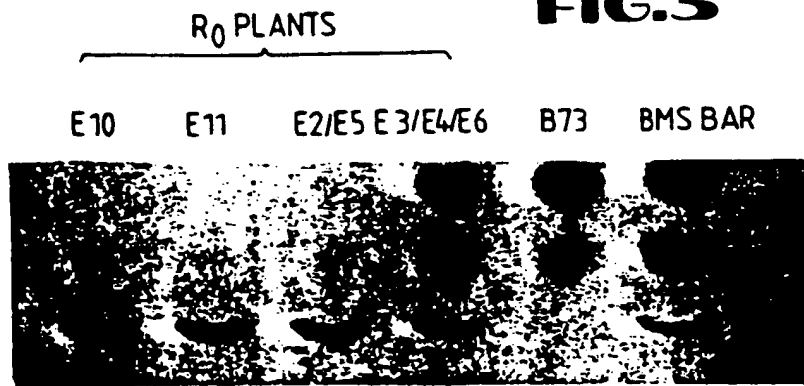
**FIG.3**



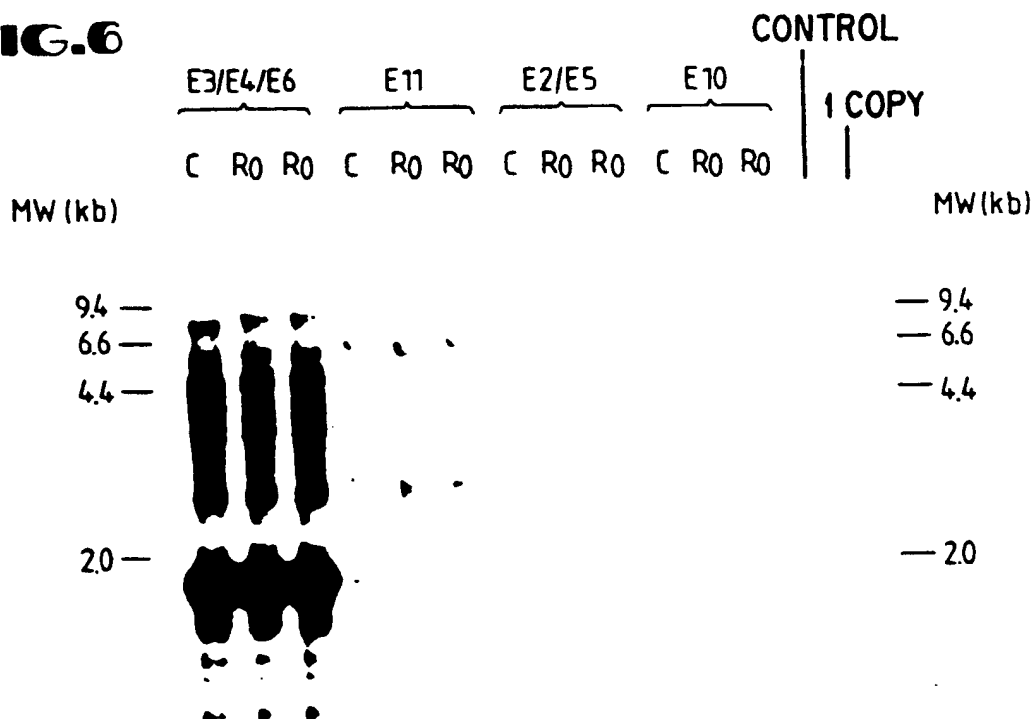
**FIG.4**



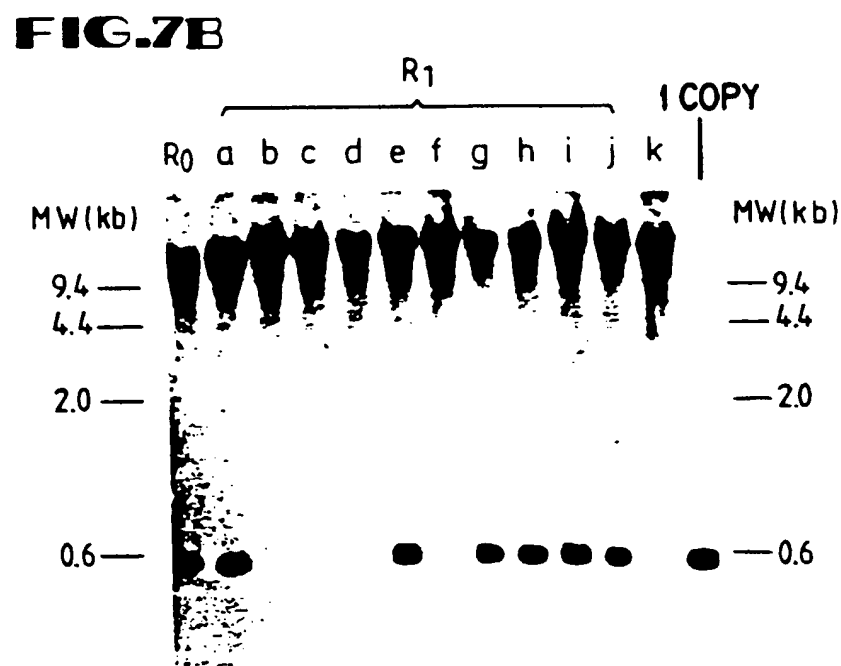
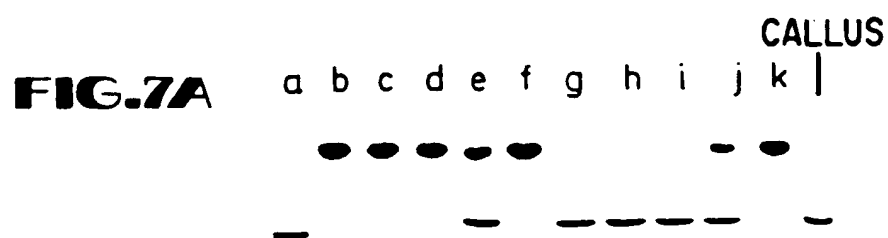
**FIG.5**



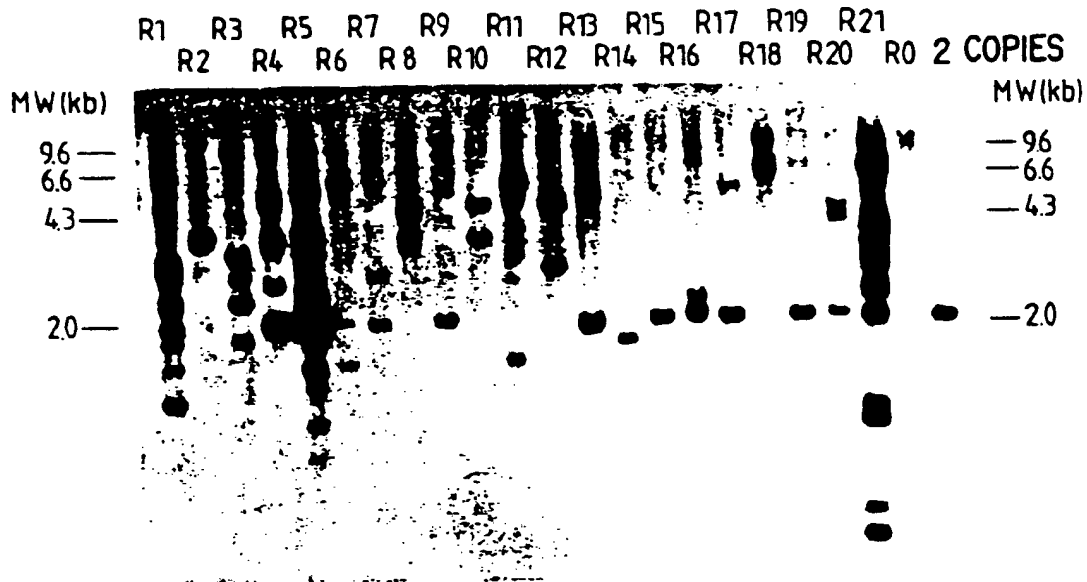
**FIG.6**



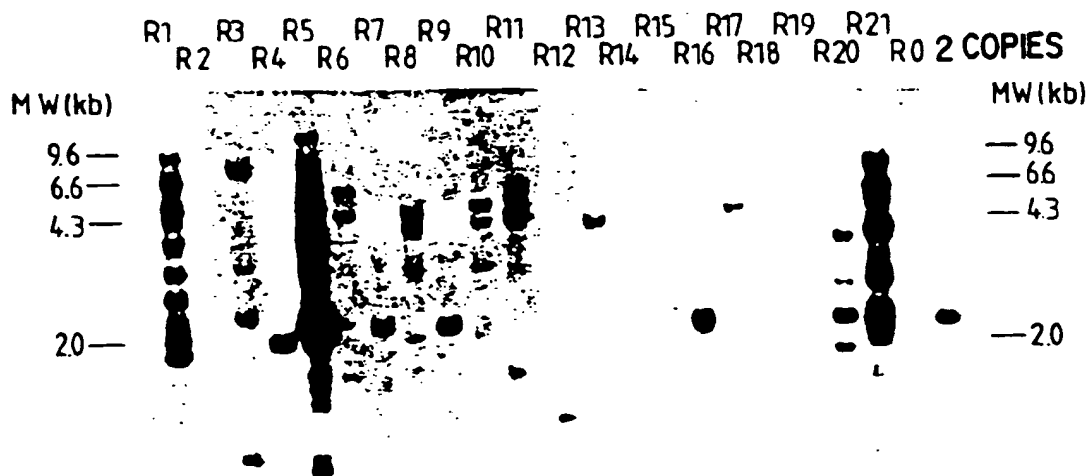




**FIG.9A**



**FIG.9B**



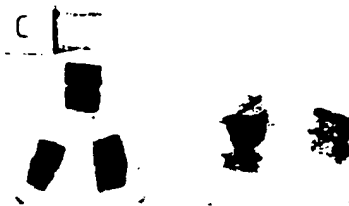
**FIG.10A**



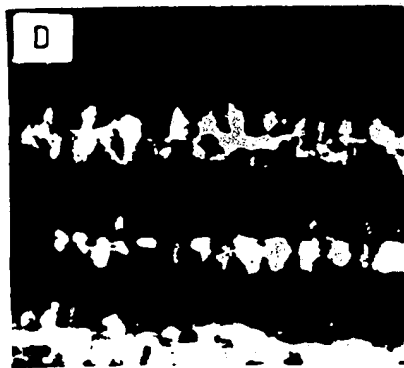
**FIG.10B**



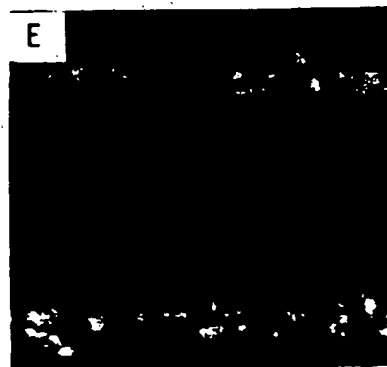
**FIG.10C**



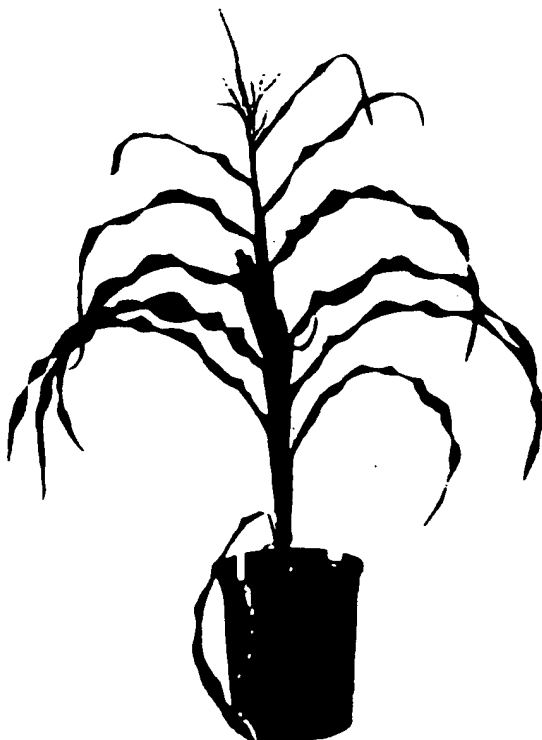
**FIG.10D**



**FIG.10E**



**FIG.11A**



**FIG.11B**



**FIG.11D**



**FIG.11E**

